

TABLE III

MOTIFS	POSITION								
	1° anchor 1	2	3	4	5	1° anchor 6	7	8	9
DR4 preferred	FMVLIIV	M	T		I	VSTCPALIM	MH		MH
deleterious				W			R		WDE
DR1 preferred	MEFLIVWY					VMATSPILC	M		AVM
deleterious		C	CH	FD	CWD		GDE	D	
DR7 preferred	MEFLIVWY	M	W	A		IVMSACTPL	M		IV (SEQ ID NO:3682)
deleterious		C		G			GRD	N	G (SEQ ID NO:3683)
DR Supermotif	MEFLIVWY					VMSTACPIL			

66

DR3 MOTIFS	1° anchor 1	2	3	1° anchor 4	5	1° anchor 6
motif a preferred	LIVMFY			D		
motif b preferred	LIVMFAY			DNQEST		KRH

Italicized residues indicate less preferred or "tolerated" residues.

Table IV: HLA Class I Standard Peptide Binding Affinity.

ALLELE	STANDARD PEPTIDE	SEQUENCE	SEQ ID NO:	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	3606	25
A*0201	941.01	FLPSDYFPSV	3607	5.0
A*0202	941.01	FLPSDYFPSV	3608	4.3
A*0203	941.01	FLPSDYFPSV	3609	10
A*0205	941.01	FLPSDYFPSV	3610	4.3
A*0206	941.01	FLPSDYFPSV	3611	3.7
A*0207	941.01	FLPSDYFPSV	3612	23
A*6802	1072.34	YVIKVSARV	3613	8.0
A*0301	941.12	KVFPYALINK	3614	11
A*1101	940.06	AVDLYHFLK	3615	6.0
A*3101	941.12	KVFPYALINK	3616	18
A*3301	1083.02	STLPETYVRR	3617	29
A*6801	941.12	KVFPYALINK	3618	8.0
A*2402	979.02	AYIDNYNKF	3619	12
B*0702	1075.23	APRTLVL	3620	5.5
B*3501	1021.05	FPFKYAAAF	3621	7.2
B51	1021.05	FPFKYAAAF	3622	5.5
B*5301	1021.05	FPFKYAAAF	3623	9.3
B*5401	1021.05	FPFKYAAAF	3624	10

Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	Sequence	SEQ ID NO:	Binding Affinity (nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	3625	5.0
DRB1*0301	DR3	829.02	YKTIAFDDEEARR	3626	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	3627	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	3628	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	3629	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	3630	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	3631	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	3632	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	3633	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	3634	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	3635	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	3636	3.5
DRB1*1501	DR2w2 β 1	507.02	GRTQDENPVVHFFK NIVTPRTPPP	3637	9.1
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	3638	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	3639	58
DRB5*0101	DR2w2 β 2	553.01	QYIKANSKFIGITE	3640	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

SE 10070501

Table VII

HCV A01 Super Motif with Binding Information

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101
ALDLEFGSF	1	165		10	13	93	
ALGFGAY	2	1265		8	14	100	
AVQWMLRLAL	3	1917		11	14	100	
CLGGRDY	4	1128	1069 62	9	11	79	0.3700
CLHRAKAVLF	5	1190		11	11	79	
CLWNRSLF	6	555		9	11	79	
CVGLVER	7	1462		8	12	86	
DEWVSLW	8	1657		9	12	86	
ELMRSEVF	9	1207		9	12	86	
ESDRRE	10	2670		8	11	79	
FLAMTRY	11	2792		8	14	100	
FLGLTRDAHF	12	1567		11	13	93	
GLFWGRLLEF	13	1552		11	12	86	
GLSAISLHSY	14	2921	1073 03	10	11	79	0.0029
GLTHDAHF	15	1569		9	13	93	
GSSGFGV	16	2641		8	11	79	
GLFIRJAY	17	2063		8	11	79	
GNAGALVAF	18	1863		9	12	86	
GVAKAVLF	19	1193		8	11	79	
GVLAAALAY	20	1670	1174 19	9	12	86	
GVHVEFPAALY	21	2619		11	14	100	
GVHVEFGNLY	22	154		11	12	86	
HEKRLIVMAY	23	696		11	11	79	
HMWNSGJOY	24	1769		11	13	93	
HQCHFGVQW	25	1910		11	11	79	
IMAKDFVF	26	2591		8	12	86	
ILVSTFGGF	27	1296		9	12	86	
IVWDYLY	28	701		8	12	86	
KSTWVPAAY	29	1241	13 2010	9	12	86	0.0130
KVLDLTCGF	30	121		10	12	86	
LEANLLW	31	2235		8	12	86	
LNNGSW	32	414		8	11	79	
LIAPLAY	33	1030		8	14	100	
LIENILGW	34	1812		9	12	86	
LISSPGSPSW	35	97		11	11	79	
LSAFLHSY	36	2922	13 0019	9	11	79	0.8100
LSRFGSPSW	37	98		10	11	79	
LTGFGADMGY	38	126		11	12	86	
LIHDAHF	39	1570		8	13	93	
LVILAGY	40	1853		8	11	79	
MLMDHF	41	2876		8	12	86	
NIVIVQVLY	42	700	1073 01	9	12	86	0.0980
NIPGGSFSLF	43	168		10	13	93	
NITVGLVDF	44	1460		10	12	86	
NINRRCQMKF	45	14		11	11	79	

Sequence	Seq. Num.	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0.101
NDXXRVW	46	1108		9	11	79	
PEVYGRK	47	1295		10	11	79	
PMGLSDHGF	48	2667		11	11	79	
PSVAATHGF	49	1261		9	14	100	
PLHGPHLLY	50	1621		11	11	79	
PMXKHEE	51	1554		9	12	86	
PDXXHLEW	52	1554		10	12	86	
QVDFSLDTE	53	1465		11	12	86	
PRHLSAI	54	2918		8	12	86	
RLAPITAY	55	1023	1174 18	9	12	86	
RMWGRHBNW	56	317		10	12	86	
RMIMTHF	57	2875		8	12	86	
RMIMTHF	58	2875		9	12	86	
RVCERKALY	59	2621	1174 21	9	14	100	
RMEDAVY	60	156	1174 17	9	12	86	
STKVPAAV	61	1242		8	12	86	
SVAATHGF	62	1262		8	14	100	
SVAATHGFAY	63	1262		11	14	100	
TIMAKRVE	64	2593		9	11	79	0.0300
TLHGPTLLY	65	1622	1073 04	10	11	79	
TLLENEGAW	66	1811		10	12	86	
TIMAKRVE	67	2589		10	11	79	
TIMKSPVI	68	1208		8	12	86	
IVDFSLDTE	69	1466		10	12	86	
VMDLTCG	70	122		9	12	86	
VLAALAAV	71	1671		8	12	86	
VLEKAVY	72	157		8	12	86	
VLDILAGY	73	1852		9	11	79	
VMGSSYGF	74	2639		8	11	79	
VMGSSYGFQY	75	2639		10	11	79	
WMNRILAF	76	1920		8	14	100	
YSKQKMEF	77	2648		9	11	79	
YINVDKRVGW	78	1106		11	11	79	
YVGDCEENVF	79	276		10	12	86	

Table VIII
HCV A02 Super Motif with Binding Information

Conservancy	Freq	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
93	13			1904	AAILRRHV	80			
86	12			1673	AALAAAYCL	81			
79	11			1250	AAQGYKVL	82			
79	11			1250	AAQGYKVLV	83			
79	11			1250	AAQGYKVLVL	84			
79	11			147	AARALAHGV	85			
79	11			147	AARALAHGVRV	86			
100	14			1264	AATLGFGA	87			
93	13			1264	AATLGFGAYM	88			
86	12			1187	AAVCTRGV	89			
79	11			1187	AAVCTRGVA	90			
79	11			1187	AAVCTRGVAK	91			
93	13			1890	AILSPGAL	92			
86	12	24.0067		1890	AILSPGALV	93	0.0014		
86	12	24.0101		1890	AILSPGALVV	94	0.0035		
100	14			150	ALAHGVRV	95			
100	14	1013.16		150	ALAHGVRVL	96	0.0037		
86	12			1737	ALGLLQTA	97			
86	12	1013.12		689	ALSTGLIHL	98	0.0160		0.2200
79	11	40.0089		1896	ALVVGVCVA	99	0.0010		
79	11			1896	ALVVGVCVAA	100			
79	11			1896	ALVVGVCVCAI	101			
86	12			1602	AOAPPSWDO	102			
79	11			1251	AQGYKVLV	103			
79	11			1251	AQGYKVLVL	104			
86	12			77	AQGYKVLVL	105			
93	13			1265	ATLGFGAYM	106			
79	11			1354	ATPGSVT	107			
79	11			1596	ATVCARQA	108			
100	14			1419	AVAYYRGL	109			
100	14	1.0486		1419	AVAYYRGLDV	110	0.0002		
79	11			1188	AVCTRGVA	111			
79	11			1188	AVCTRGVAKA	112			
79	11			1188	AVCTRGVAKAV	113			
100	14			1917	AVQWMNRL	114			
100	14	1174.09		1917	AVQWMNRLI	115	0.0001		
100	14			1917	AVQWMNRLIA	116			
93	13			1903	CAAILRRHV	117			
79	11			1530	CAWYELTPA	118			
86	12	1.0510		2941	CLRKLGPPL	119	0.0002		
86	12			739	GLWMMILLI	120			
79	11			1653	CMSADLEV	121			

Conservancy	Freq.	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
79	11	1.0131		1653	CMSADLEW	122	0.0067		
79	11			1653	CMSADLEWT	123			
79	11			1128	CTCGSSDL	124			
79	11			1128	CTCGSSDLYL	125			
79	11			1128	CTCGSSDLYLV	126			
79	11			1190	CTRGVAKA	127			
79	11			1190	CTRGVAKAV	128			
79	11			555	CTWMNSTGFT	129			
79	11	1.0487		1462	CVTQTVDFSL	130	0.0006		
86	12			1527	DAGCAWYEL	131			
79	11			1574	DAHFLSQT	132			
100	14			1855	DILAGYGA	133			
86	12			1855	DILAGYGAGV	134	0.0002		
79	11	1.0495		1855	DILAGYGAGVA	135			
79	11			279	DLCGSVFL	136			
86	12	939.11		279	DLCGSVFLV	137	0.0007		
79	11			1657	DLEVTST	138			
86	12	1.0490		1657	DLEVTSTW	139	0.0002		
86	12			1657	DLEVTSTWWL	140			
86	13			2617	DLGVRVCEKM	141			
93	13			2617	DLGVRVCEKMA	142			
79	11			132	DLMGYIPL	143			
79	11	1013.1002		132	DLMGYIPLV	144	0.0630	0.0009	0.0490
79	11			132	DLMGYIPLVGA	145			
79	11			2412	DLSDGSWST	146			
79	11	1.0499		2412	DLSDGSWSTV	147	0.0008		
79	11			1883	DLVNLLPA	148			
79	11			1883	DLVNLLPAI	149	0.0001		
79	11	14.0052		1883	DLVNLLPAIL	150	0.0001		
79	11	1.0891		2772	DLVWICESA	151			
79	11			1134	DLYLVTRHA	152	0.0001		
86	12	24.0074		1134	DLYLVTRHADV	153			
86	12			321	DMMMNWSPT	154			
86	12			1339	DQAEATAGA	155			
86	12			1339	DQAEATAGARL	156			
86	12			1339	DQAEATAGARLV	157			
86	12			994	DTAACGDI	158			
86	12			994	DTAACGDII	159			
86	12			124	DTLTCGFA	160			
86	12			124	DTLTCGFADL	161			
86	12			124	DTLTCGFADLM	162			
86	12			2673	DTRCFDST	163			
93	13								

Conservancy	Freq	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
93	13			2673	DTRCFDSTV	164			
93	13			2673	DTRCFDSTVT	165			
86	12	1174.01		21	DVKFPGGGQI	166	0.0001		
86	12			21	DVKFPGGGQV	167			
79	11			750	EAALENLV	168			
100	14			2794	EAMTRYSA	169			
86	12			2237	EANLLWROEM	170			
93	13			1377	EIPFYGKA	171			
93	13	1174.07		1377	EIPFYGKAI	172	0.0001		
100	14	1.0506		2814	ELITSCSSNV	173	0.0002		
79	11			666	ELSPLLST	174			
79	11			666	ELSPLLSTT	175			
86	12	1174.11		2245	EMGGNITRV	176	0.0003		
86	12			1731	EOFKQKAL	177			
86	12			1731	EOFKQKALGL	178			
86	12			1731	EOFKQKALGLL	179			
86	12			1342	ETAGARLV	180			
86	12			1342	ETAGARLVW	181			
86	12			1342	ETAGARLVVL	182			
86	12			1342	ETAGARLVLA	183			
86	12			1207	ETMRSPV	184			
86	12			1207	ETMRSPVFT	185			
86	12	1.0132		1659	EWSTWV	186	0.0001		
86	12	1.0491		1659	EWSTWVL	187	0.0004		
86	12			1659	EVTSTWLV	188			
93	13			130	FADLMGYI	189			
79	11			130	FADLMGYIPL	190			
79	11			130	FADLMGYIPLV	191			
100	14			1927	FASRGNHV	192			
86	12			1927	FASRGNHVSPT	193			
100	14			1773	FISGIQYL	194			
100	14	40.0082		1773	FISGIQYLA	195	0.1000		
100	14			1773	FISGIQYLAGL	196			
79	11			1304	FLADGGCSGGA	197			
86	12	1.0818		177	FLALLSCL	198	0.0046		
86	12			177	FLALLSCLT	199			
93	13	1090.18		728	FLLADARV	200	0.2800	0.0480	0.0670
86	12			1228	FQVAHLHA	201			
86	12			1228	FQVAHLHAPT	202			
79	11			2646	FOYSPGQV	203			
100	14			2792	FTEAMTRYSA	204			
93	13			1567	FTGLTHIDA	205			

Conservancy	Freq.	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
93	13			512	FTPSPVV	206			
93	13			512	FTPSPVVG	207			
93	13			512	FTPSPVVGTT	208			
79	11			684	FTTLPALST	209			
79	11			684	FTTLPALSTGL	210			
79	11			146	GAARALAHGV	211			
86	12			992	GADTAACGDI	212			
86	12			992	GADTAACGDII	213			
86	12			1861	GAGVAGAL	214			
86	12			1861	GAGVAGALV	215			
86	12			1861	GAGVAGALVA	216			
86	12			350	GAHWGVLA	217			
79	11			1895	GALVGVV	218			
79	11			1895	GALVGVVCA	219			
79	11			1895	GALVGVVCAA	220			
86	12			1345	GARLVLA	221			
79	11			1345	GARLVVLT	222			
79	11			1345	GARLVVLATA	223			
79	11			1345	GARLVVLATAT	224			
100	14	24.0061		1916	GAVQWMNRL	225	0.0001		
100	14			1916	GAVQWMNRLI	226			
100	14			1916	GAVQWMNRLIA	227			
100	14			1333	GIGTVLDOA	228			
100	14			1333	GIGTVLDOAET	229			
100	14			1776	GIQYLAGL	230			
100	14			1776	GIQYLAGLST	231			
100	14			1776	GIQYLAGLSTL	232			
79	11			1425	GLDVSVIPT	233			
93	13	1.0126		1552	GLPVCCOHL	234	0.0001		
79	11			968	GLRDLAVA	235			
79	11	1.0114		968	GLRDLAVAV	236	0.0034		
100	14			1782	GLSTLPGNPA	237			
79	11			1782	GLSTLPGNPAL	238			
93	13	1.0488		1569	GLTHIDAHFL	239	0.0007		
93	13			28	GQVGGVYL	240			
93	13			28	GQVGGVYLL	241			
79	11			2063	GTFPINAYT	242			
79	11			2063	GTFPINAYTT	243			
100	14			1335	GTVLDOAET	244			
100	14			1335	GTVLDOAETA	245			
86	12			1863	GVAGALVA	246			
79	11			1081	GVCWTYHGA	247			

Conservancy	Freq.	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
86	12			1670	GVLAALAA	248			
86	12			1670	GVLAALAAAYCL	249			
79	11	1.0099		161	GVNYATGNL	250	0.0001		
86	12			45	GVRATRKT	251			
100	14			2619	GVRVCEKM	252			
100	14			2619	GVRVCEKMA	253			
100	14	1.0504		2619	GVRVCEKMAL	254	0.0002		
93	13	1.0095		154	GVRVLEDGV	255	0.0001		
79	11			1900	GVVCAAIL	256			
100	14			1234	HPTGSGKST	257			
100	14			1572	HIDAHLSQT	258			
86	12	939.14	*	696	HLHQNVDV	259	0.0100	0.0014	0.5400
79	11			1719	HLPIEQGM	260			
93	13	1174.08	*	1769	HMWNFISGI	261	0.3300	0.0004	0.1300
79	11			698	HQNVDOYVL	262			
79	11			222	HTPGCVPCV	263			
86	12			2855	HTPVNSWL	264			
86	12			2855	HTPVNSWLGNI	265			
79	11			1910	HVGPGEA	266			
79	11			1910	HVGPGEAV	267			
86	12			1933	HVSPTHYV	268			
100	14			1925	IAFASRGHNV	269			
79	11	1073.06	*	1856	ILAGYGAGV	270	0.0430	0.0300	2.0000
79	11	40.0140		1856	ILAGYGAGVA	271	0.0002		
86	12			1816	ILGGWVAA	272			
86	12	1090.16	*	1816	ILGGWVAAQL	273	0.0430	0.0024	0.0190
86	12			1816	ILGGWVAAQLA	274			
86	12			1331	ILGIGTVL	275			
86	12			1331	ILGIGTVLDQA	276			
93	13			1891	ILSPGALV	277			
93	13	24.0065	*	1891	ILSPGALW	278	0.0210	0.0004	0.3700
93	13			1891	ILSPGALWGV	279			
79	11	1.0500		2591	IMAKNEVFCV	280	0.0088		
100	14			1777	IQYLAGLST	281			
100	14			1777	IQYLAGLSTL	282			
86	12			2250	ITRVESENKV	283			
86	12			2250	ITRVESENKVV	284			
100	14			2816	ITSCSSNV	285			
100	14			2816	ITSCSSNVSV	286			
100	14			2816	ITSCSSNVSVVA	287			
86	12			989	ITWGADTA	288			
86	12			989	ITWGADTAA	289			

Conservancy	Freq.	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
79	11			1296	ITYSTYKFL	290			
79	11			1296	ITYSTYKFLA	291			
79	11			2613	IVFDLGV	292			
79	11	1.0503		2613	IVFDLGV RV	293	0.0016		
93	13			30	IVGGVLL	294			
86	12			1736	KALGLLOT	295			
86	12			1736	KALGLLQTA	296			
86	12			2625	KMALYDVV	297			
86	12			1734	KOKALGLL	298			
86	12			1734	KOKALGLLOT	299			
86	12			1734	KOKALGLLQTA	300			
86	12			121	KVIDTLTCGFA	301			
86	12			1255	KVLVNPSV	302	0.0048		
100	14	1174.05		1255	KVLVNPSVA	303			
100	14			1255	KVLVNPSVAA	304			
100	14			1244	KVPAAYAA	305			
79	11	24.0068		1672	LAALAAAYCL	306	0.0011		
86	12			1305	LADGGCSGA	307			
79	11			1729	LAEOFKQKA	308			
86	12			1729	LAEOFKQKAL	309			
86	12			1857	LAGYGAGV	310			
79	11			1857	LAGYGAGVA	311			
79	11			1857	LAGYGAGVAGA	312			
100	14			151	LAHGVRL	313			
86	12			179	LALLSCLT	314			
79	11			972	LAVAVEPV	315			
100	14			1924	LIAFASRGNHV	316			
100	14	1.0147		2815	LITSCSSNV	317	0.0004		
100	14			2815	LITSCSSNVSV	318			
79	11	1.0826		2612	LVFPDLGV	319	0.0002		
79	11			2612	LVFPDLGV RV	320			
86	12			178	LLALLSCL	321			
86	12			178	LLALLSCLT	322			
100	14	24.0071	*	726	LLFLLADA	323	0.0230	0.0150	0.0220
93	13			726	LLFLLADARV	324			
12	12	1073.05	*	1812	LLFNILGGWV	325	1.2000	0.0380	3.1000
86	12			1812	LLFNILGGWVA	326			
93	13			729	LLADARV	327			
93	13	24.0102		1887	LLPAILSPGA	328	0.0061		
93	13			1887	LLPAILSPGAL	329			
93	13	24.0066		36	LLPRGPRL	330	0.0025		
93	13			36	LLPRGPRLGV	331			

Conservancy	Freq	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
86	12			2240	LLWRQEMGGNI	332			
93	13			1629	LLYRLGAV	333			
79	11			133	LMGYIPLV	334			
79	11			133	LMGYIPLVGA	335			
86	12			2761	LQDCTMLV	336			
86	12			126	LTCGFADL	337			
86	12			126	LTCGFADLM	338			
100	14			2180	LTDP SHIT	339			
100	14			2180	LTDP SHITA	340			
86	12			1052	LTGRDKQV	341			
93	13			1570	LTHIDAHFL	342			
93	13			2176	LTSM LTPSHI	343			
79	11			2738	LTSCGNT	344			
79	11			2738	LTSCGNTL	345			
79	11			2738	LTSCGNTLT	346			
86	12			1591	LVAYQATV	347			
86	12	40.0133		1591	LVAYQATVCA	348	0.0002		
79	11	40.0139		1853	LVDILAGYGA	349	-0.0001		
86	12			1667	LVGGVLA	350			
86	12	1.0133		1667	LVGGVLAAL	351	0.0003		
86	12			1667	LVGGVLAALA	352			
86	12			1667	LVGGVLAALAA	353			
100	14			1257	LVLNPSVA	354			
100	14			1257	LVLNPSVAA	355			
100	14			1257	LVLNPSVAAT	356			
100	14			1257	LVLNPSVAATL	357			
79	11			1884	LVNLLPAI	358			
79	11	1.0825		1884	LVNLLPAIL	359	0.0002		
86	12			1137	LVTRHADV	360			
79	11	14.0048		1137	LVTRHADVI	361	0.0001		
79	11			1137	LVTRHADVIPV	362			
79	11			1897	LVVGWCA	363			
79	11			1897	LVVGWVCAA	364			
79	11	40.0141		1897	LVVGWVCAAI	365	0.0011		
79	11			1897	LVVGWVCAAIL	366			
79	11			2773	LVVICA	367			
86	12			1348	LVVLATAT	368			
86	12	24.0069		2592	MAKNEVFCV	369	0.0022		
100	14			2179	MLTDP SHI	370			
100	14	24.0062		2179	MLTDP SHIT	371	0.0002		
100	14			2179	MLTDP SHITA	372			
93	13			322	MMMNWSPT	373			

Conservancy	Freq.	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
93	13			1418	NAVAYYRGL	374			
93	13			1418	NAVAYYRGLDV	375			
86	12			2068	NAYTTGPCT	376			
86	12			1815	NILGGWVA	377			
86	12			1815	NILGGWAA	378			
86	12			1815	NILGGWAAQL	379			
93	13			1282	NIRTVRT	380			
79	11	1174.06		1282	NIRTVRTI	381	0.0001		
79	11			1282	NIRTVRTIT	382			
79	11			1282	NIRTVRTITT	383			
86	12			2249	NITRVESENKV	384			
86	12			700	NIVDVQYL	385			
86	12			118	NLGKVIDT	386			
86	12			118	NLGKVIDTL	387			
86	12	939.18		118	NLGKVIDTLT	388	0.0006		
93	13			1886	NLLPAILSPGA	389			
86	12			2239	NLLWRQEM	390			
93	13	1174.02	*	168	NLPGCSFSI	391	0.0041		
93	13			168	NLPGCSFSIFL	392			
86	12			1460	NTCVTQTV	393			
93	13			416	NTNGSWHI	394			
86	12			14	NTNRRPODV	395			
93	13			1889	PAILSPGA	396			
93	13			1889	PAILSPGAL	397			
86	12			1889	PAILSPGALV	398			
86	12			1889	PAILSPGALVV	399			
86	12			688	PALSTGLI	400			
86	12			688	PALSTGLIHL	401			
79	11			2609	PARLIVFIDL	402			
79	11			2066	PINAYTTGPCT	403			
79	11			1295	PITYSTYGKFL	404			
93	13			2403	PLEGERGDPDL	405			
79	11	1.0093		143	PLGGAARA	406	0.0001		
79	11			143	PLGGAARAL	407			
79	11			143	PLGGAARALA	408			
93	13			1628	PLLYRLGA	409			
93	13	1.0130		1628	PLLYRLGAV	410	0.0001		
79	11			2667	PMGFSYDT	411			
79	11			2807	POPEYDLEL	412			
79	11			2807	POPEYDLELI	413			
79	11			2807	POPEYDLELIT	414			
93	13			7	PORKTKRNT	415			

Conservancy	Freq	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
86	12			109	PTDPRRRSRNL	416			
79	11			1473	PTFTIETT	417			
79	11			1473	PTFTIETT	418			
100	14			1236	PTSGGKST	419			
93	13			1236	PTSGGKSTKV	420			
86	12			1936	PTHVPESDA	421			
86	12			1936	PTHVVPESDAA	422			
79	11			1621	PTLHGPTPL	423			
79	11			1621	PTLHGPTPL	424			
79	11			2870	PTLWARM	425			
79	11			2870	PTLWARMIL	426			
79	11			2870	PTLWARMILM	427			
79	11			2870	PTLWARMILMT	428			
100	14			1626	PTPLLYRL	429			
93	13			1626	PTPLLYRLGA	430			
93	13			1626	PTPLLYRLGAV	431			
100	14	1174.13		2857	PVNSWLGNI	432	0.0001		
100	14	1174.14		2857	PVNSWLGNIH	433	0.0001		
86	12			2857	PVNSWLGNIIM	434			
79	11			2318	PVHGCPL	435			
93	13	1.0471		508	PVYCFTSPV	436	0.0004		
93	13			508	PVYCFTSPVV	437			
86	12			1340	QAETAGARL	438			
86	12			1340	QAETAGARLV	439			
86	12			1340	QAETAGARLVV	440			
86	12			1603	QAPPSWDQM	441			
93	13			1595	QATVCARA	442			
79	11			1595	QATVCARAQA	443			
93	13			29	QIVGGVYL	444			
93	13	1.0088		29	QIVGGVYLL	445	0.0015		
86	12			336	QLLRIPQA	446			
86	12	1.0497		2164	QLPCEPEPDV	447	0.0002		
79	11			2210	QLSAPSLKA	448			
79	11			2210	QLSAPSLKAT	449			
86	12			1465	QTVDFSLDPT	450			
86	12			1229	QVAHLHAPT	451			
86	12			1186	RAAVCTRGV	452			
79	11			1186	RAAVCTRGVA	453			
100	14	24.0063		149	RALAHGVRV	454	0.0001		
100	14			149	RALAHGVRVL	455			
86	12			2733	RASGVLTT	456			
79	11			43	RLGVRATRKT	457			

Conservancy	Freq	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
79	11	1090.21	.	2918	RLHGLSAFSL	458	0.0280	0.0055	0.0160
79	11			2611	RLVFPDL	459			
79	11	1090.22	.	2611	RLVFPDLGV	460	0.0890	0.0110	1.0000
79	11			1618	RLKPTLHGPT	461			
86	12			1029	RLAPITA	462			
86	12			1347	RLVVLATA	463			
86	12			1347	RLVVLATAT	464			
100	14			619	RLWHYPCT	465			
86	12			317	RMAWDMM	466			
93	13			635	RMVVGVEHRL	467			
86	12			2243	ROEMGGNI	468			
86	12			2243	ROEMGGNIT	469			
86	12			2243	ROEMGGNITRV	470			
79	11			1284	RTGVRTIT	471			
79	11			1284	RTGVRTITT	472			
100	14			2621	RVCEKMAL	473			
86	12			2621	RVCEKMALYDV	474			
86	12			2252	RVESENKV	475	0.0001		
86	12	1.0138		2252	RVESENKV	476			
79	11			2100	RVGDFRV	477			
86	12			156	RVLEDGVNYA	478			
86	12			156	RVLEDGVNYAT	479			
86	12			2833	RVVYLTRDPT	480			
79	11			1655	SADLEVVT	481			
79	11			1655	SADLEVVTST	482			
79	11			2212	SAPSLKAT	483			
79	11			2212	SAPSLKATCT	484			
93	13			2207	SASOLSAPSL	485			
100	14			175	SIFLLALL	486			
86	12			175	SIFLLALLSCL	487			
100	14			1470	SLDPTFTI	488			
86	12			1470	SLDPTFTIET	489			
79	11			1470	SLDPTFTIETT	490			
79	11	1174.15		2926	SLHSYSPGEI	491	0.0008		
86	12	1.0478		1051	SLTGRDNQV	492	0.0002		
100	14	1174.10		2178	SMLTDPISHI	493	0.0053		
100	14			2178	SMLTDPISHIT	494			
100	14			2178	SMLTDPISHITA	495			
86	12			2163	SQLPCEPEPDV	496			
93	13			2209	SQLSAPSL	497			
79	11			2209	SQLSAPSLKA	498			
79	11			2209	SQLSAPSLKAT	499			

Conservancy	Freq	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
93	13			56	SOPRRROPI	500			
86	12			1242	STKVPAAYA	501			
79	11			1242	STKVPAAYAA	502			
100	14			1784	STLPGNPA	503			
79	11	40.0083		1784	STLPGNPAI	504	0.0007		
79	11			2	STNPKPQPKT	505			
86	12			1663	STWLVGGV	506			
86	12			1663	STWLVGGVL	507			
86	12			1663	STWLVGGVLA	508			
86	12			1299	STYGKFLA	509			
100	14			1262	SVAATLGFGA	510			
86	12	1.0124		1455	SVIDCNTCV	511	0.0088		
86	12			1455	SVIDCNTCVT	512			
86	12			995	TAACGDII	513			
86	12			1343	TAGARLVV	514			
86	12			1343	TAGARLVVL	515			
86	12			1343	TAGARLVVLA	516			
79	11			1343	TAGARLVLAT	517			
79	11			2852	TARHTPVNSWL	518			
79	11			2590	TIMAKNEV	519			
93	13			1266	TLGFGAYM	520			
86	12			1266	TLGFGAYMSKA	521			
79	11			1622	TLHGPTPL	522	0.0070		
79	11	1.0129		1622	TLHGPTPLL	523			
86	12			1811	TLLFNILGGW	524			
79	11	1.0108		686	TLPALSTGL	525	0.0003		
79	11	1174.03		686	TLPALSTGLI	526	0.0004		
79	11			1785	TLPGNPAI	527			
86	12	1.0092		125	TLTCGFADL	528	0.0003		
86	12			125	TLTCGFADLM	529			
79	11			2871	TLWARMIL	530			
79	11			2871	TLWARMILM	531			
79	11			2871	TLWARMILMT	532			
86	12			1209	TMRSVPFT	533			
86	12			1464	TQTVDFSL	534			
86	12			1464	TQTVDFSLDPT	535			
79	11			2589	TTIMAKNEV	536			
79	11			685	TTLPALST	537			
79	11			685	TTLPALSTGL	538			
79	11			685	TTLPALSTGLI	539			
86	12			1208	TTMRSPVFT	540			
79	11			2739	TTSCGNL	541			

Conservancy	Freq.	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
79	11			2739	TTSCGNLT	542			
79	11			1597	TVCARAGA	543			
86	12			1466	TVDFSLDPT	544			
86	12			1466	TVDFSLDPTFT	545			
100	14			1336	TVLDOAET	546			
100	14			1336	TVLDOAETA	547			
86	12			1336	TVLDOAETAGA	548			
100	14			1263	VAATLGFGA	549			
93	13			1263	VAATLGFGAYM	550			
86	12			1230	VAHLHAPT	551			
86	12			1440	VATDALMT	552			
86	12	40.0071		1592	VAYOATVCA	553	0.0005		
79	11			1592	VAYOATVCAR	554			
100	14	24.0064		1420	VAYYRGLDV	555	0.0001		
100	14			1420	VAYYRGLDVSV	556			
86	12			1456	VIDCNTCV	557			
86	12			1456	VIDCNTCVT	558			
86	12			1456	VIDCNTCVTQT	559			
86	12			122	VIDTLTCGFA	560			
86	12	1090.20		1671	VLAALAAAYCL	561	0.0500	0.0087	0.0047
93	13			1521	VLECECYDA	562			
79	11			1521	VLECECYDAGCA	563			
100	14			1337	VLDQAETA	564			
86	12			1337	VLDQAETAGA	565			
86	12			157	VLEDGVNYA	566			
86	12			157	VLEDGVNYAT	567			
100	14			1258	VLNPSVAA	568			
100	14			1258	VLNPSVAAT	569			
100	14	1.0483		1258	VLNPSVAATL	570	0.0015		
79	11			2737	VLTTSCGNT	571			
79	11	1.0505		2737	VLTTSCGNLT	572	0.0002		
79	11			2737	VLTTSCGNLT	573			
79	11			1852	VLVDILAGYGA	574			
86	12			1666	VLVGGVLA	575			
86	12	24.0075		1666	VLVGGVLAA	576	0.0270	0.0130	0.3100
86	12	1.0492		1666	VLVGGVLAAL	577	0.0084		
86	12			1666	VLVGGVLAALA	578			
100	14			1256	VLVLNPSV	579			
100	14	24.0072		1256	VLVLNPSVA	580	0.0009		
100	14			1256	VLVLNPSVAA	581			
100	14			1256	VLVLNPSVAAT	582			
79	11			2600	VOPEKGRKPA	583			

HCV A02 Super Motif With Binding Information

Conservancy	Freq.	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
100	14			1918	VQWMNRLI	584			
100	14			1918	VQWMNRLIA	585			
100	14			1918	VQWMNRLIAFA	586			
86	12			1463	VTQTVDFSL	587			
79	11			1138	VTRHADVI	588			
79	11			1138	VTRHADVIPV	589			
86	12			1661	VTSTWVLV	590			
86	12			1661	VTSTWLVGGV	591			
79	11			1439	VVATDALM	592			
79	11			1439	VVATDALMT	593			
79	11			1901	WCAAILRRHV	594			
79	11			1898	WGVVCAA	595			
79	11			1898	WGVVCAA	596			
79	11			1898	WGVVCAAIL	597			
86	12			1660	WTSTWVL	598			
86	12	1.0823		1660	VTSTWVLV	599	0.0003		
86	12	24.0070		1766	WAKHWNFI	600	0.0001		
86	12			76	WAQPGYPWPL	601			
86	12			2873	WARMILMT	602			
79	11			2297	WARPDPNPPL	603			
100	14	24.0073		1920	WMNRLIAFA	604	0.0410	0.0330	3.0000
79	11			557	WMNSTGFT	605			
86	12			1665	WLVGGVL	606			
86	12	40.0075		1665	WLVGGVLA	607	0.0005		
86	12	40.0135		1665	WLVGGVLA	608	0.0015		
86	12			1665	WLVGGVLAAL	609			
79	11			1249	YAAQGYKV	610			
79	11			1249	YAAQGYKVL	611			
79	11			1249	YAAQGYKVLV	612			
79	11			1249	YAAQGYKVLVL	613			
79	11	1.0817		136	YPLVGAPL	614	0.0050		
100	14			1779	YLAGLSTL	615			
86	12	1.0479		1165	YKGSSTGGL	616	0.0002		
86	12			1165	YKGSSTGGLL	617			
93	13	1073.07		35	YLLPRRGPRL	618	0.0400	0.0007	0.0220
79	11			2836	YLTRDPTT	619			
86	12			1590	YLVAYQAT	620			
86	12	1013.02		1590	YLVAYQATV	621	0.2500	0.1100	0.6300
86	12			1590	YLVAYQATVCA	622			
86	12	1.0119		1136	YLVTRHADV	623	0.0110	0.0021	2.8000
79	11			1136	YLVTRHADVI	624			
93	13			1594	YQATVCARA	625			

Conservancy	Freq	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
79	11			1594	YQATVCARAQ	626			
79	11			1106	YTNVDQDL	627			
79	11			1106	YTNVDQDLV	628			
86	12	1.0100		276	YWGDLGGSV	629	0.0018		
86	12			276	YWGDLGGSVFL	630			
93	13	1.0107		637	YGGVEHRL	631	0.0008		
86	12			1939	YVPESDAA	632			
86	12			1939	YVPESDAAA	633			
86	12			1939	YVPESDAAARV	634			

Table IX
ICV A03 Super Motif (With Binding Information)

Conservancy	Freq	Position	Sequence	SeqID Num	Filed	Peptide	A*0301	A*1101	A*3101	A*3301	A*6801
86	12	647	AACHWTRGER	635	.	24 0103	0 0003	0 0140	0 0450	0 0055	0 0018
79	11	147	AARALAHGVR	636	.						
79	11	1187	AAVCIRGVAK	637	.						
79	11	2208	ASQLSAPSLK	638	.						
86	12	1265	ATLFGAYMSK	639	.						
79	11	48	ATRKTSER	640	.						
79	11	1188	AVCTRGVAK	641	.	1090 23	0 0260	0 0250	0 0011	0 0004	0 0001
86	12	2941	CLRKLGVPPLR	642	.						
79	11	555	CTWMNSTGFTK	643	.	3 0438	0 7600	0 7500			
79	11	2599	CVOPEKGGR	644	.	1 0961	0 0008	0 0005			
79	11	2599	CVOPEKGGR	645	.	1 0501	0 0011	0 0008			
100	14	1574	DAHFLSOTK	646	.	24 0076	0 0003	0 0005			
93	13	2617	DLGVRVCEK	647	.	1 0144	0 0003	0 0002	0 0006	0 0440	0 0002
79	11	1143	DVIPVRRR	648	.						
86	12	2245	EMSGNTR	649	.						
86	12	2596	FVFCVQPEK	650	.	1090 24	0 0008	0 0270	0 0003	0 0005	0 4500
100	14	728	FLLADAR	651	.						
79	11	146	GAARALAHGVR	652	.						
100	14	1916	GAVQWMNR	653	.						
79	11	3037	GYLLPNR	654	.						
79	11	1004	GLVPSARR	655	.						
86	12	1131	GSSDLVLTIR	656	.						
86	12	1863	GVAGALVAFK	657	.	1073 10	0 3900	1 4000	0 0055	0 0011	0 0680
79	11	3035	GVGYLLPNR	658	.	1090 25	0 0014	0 0140	0 1500	0 0130	0 0007
79	11	45	GVRATRTSER	659	.						
79	11	1900	GVVCAAILR	660	.						
79	11	1900	GVVCAAILR	661	.						
93	13	33	GYLLPRR	662	.						
93	13	33	GYLLPRR	663	.						
79	11	1141	HADVIPR	664	.						
79	11	1141	HADVIPRR	665	.						
79	11	1141	HADVIPRRR	666	.						
100	14	1234	HAPTSKGSK	667	.						
93	13	1234	HAPTSKGSK	668	.						
100	14	1572	HIDAHFLSOTK	669	.						
86	12	1232	HIHAPTSKGK	670	.	1073 16	0 5900	0 0024	0 0005	0 0006	0 0028
100	14	1395	HLIFCHSK	671	.						
100	14	1395	HLIFCHSKK	672	.	1090 26	0 0250	0 0006	0 0003	0 0004	0 0010
100	14	1395	HLIFCHSKKK	673	.	1073 12	0 0260	0 0002	0 0009	0 0006	0 0001
79	11	2928	HSYSPGEINR	674	.						
79	11	222	HTPGCVPCVR	675	.	1 1061	0 0004	0 0012	0 0007	0 0006	0 0092
86	12	2250	ITRVESENK	676	.	1 0137	0 0150	0 0079			
86	12	1296	ITYSTYK	677	.						
79	11	2613	IVFPNLGVR	678	.	1 0962	0 0036	0 0044			
93	13	30	IVGGVLLPR	679	.	1 1060	0 0008	0 0056			
93	13	30	IVGGVLLPRR	680	.						
86	12	2944	KLGVPPLR	681	.						
86	12	10	KTKRNTNR	682	.						
86	12	10	KTKRNTNR	683	.	24 0085	0 0110	0 0100			
93	13	51	KTSERSQPR	684	.	1 0952	0 1600	0 0640	0 2700	0 0160	0 0550
86	12	1729	KTSERSQPRGR	685	.						
86	12		LAEOFKOK	686	.						

Conservancy	Freq	Position	Sequence	SeqID Num	Filed	Peptide	A*0301	A*1101	A*3101	A*3301	A*6801
86	12	2235	LEANLLWR	687		1 0959	0 0008	0 0005	0 0018	0 0069	0 0008
100	14	1396	LIFCHSKK	688							
100	14	1396	LIFCHSKK	689		1 0123	0 5400	0 1900	0 0071	0 0012	0 0240
79	11	2612	LVFPLGVR	690		1 1066	0 0003	0 0001			
100	14	726	LLFLLADAR	691		1090 28					
93	13	36	LLPRGR	692							
86	12	97	LLSPGR	693							
79	11	1591	LVAYQATVCAR	694							
79	11	1	MSINPKPOR	695							
79	11	1	MSINPKPOR	696							
86	12	2249	NITRVESEIK	697		1 0498	0 0010	0 0062			
79	11	14	NINRRPOOVK	698		2 0168	0 0010	0 0007			
79	11	1295	PITYSTYCK	699							
79	11	2667	PMGFSYDTR	700							
93	13	514	PSVWVGTTDR	701							
79	11	1607	PSWDMWK	702							
86	12	109	PTDPRRSR	703		1 0954	0 0008	0 0005			
93	13	1236	PTGSGKSTK	704		1 0121	0 0002	0 0001	0 0006	0 0006	0 0002
93	13	516	PVWVGTTDR	705		1 0956	0 0008	0 0005			
86	12	1340	QAEATAGAR	706							
93	13	29	QVGGVLLPR	707							
86	12	289	QLFTSPR	708							
79	11	289	QLFTSPR	709		1 0955	0 7500	0 0330	0 0290	0 0077	3 1000
79	11	2210	QLSAPSLK	710							
79	11	1186	RAAVCTRGVAK	711							
100	14	149	RALAHGVR	712							
79	11	47	RATRTSER	713							
79	11	43	RLGVRATR	714							
79	11	43	RLGVRATR	715		1073 11	0 9400	0 0290	0 0420	0 0004	0 0001
100	14	1923	RLIAFASR	716							
79	11	2611	RLVFPDLGVR	717							
100	14	635	RMVGGVEHR	718		1073 13	0 7200	0 0200	0 1900	0 0030	0 0045
93	13	55	RSOPRGR	719							
79	11	2207	SASQLSAPSLK	720		24 0089	0 0003	0 0044			
86	12	1132	SSDLYLVR	721							
79	11	2	STNPKPOR	722							
79	11	2	STNPKPOR	723							
79	11	2	STNPKPOR	724							
86	12	1266	TLGFGAYMSK	725		1073 14	0 0810	0 0610	0 0005	0 0013	0 0009
79	11	1622	TUHGPTLLYR	726							
93	13	52	TSESROR	727							
86	12	52	TSESROR	728		24 0107	0 0003	0 0001			
86	12	52	TSESROR	729							
86	12	1050	TSLTGRDK	730							
86	12	1864	VAGALVAFK	731		24 0000	0 2400	0 8900	0 0048	0 0025	0 0310
79	11	1592	VAYQATVCAR	732		1 1064	0 0005	0 0038	0 0680	0 0720	0 0280
86	12	1337	VLDQAEATAGAR	733							
79	11	1138	VTRHADVIPVR	734							
79	11	1901	VVCAAILR	735							
79	11	1901	VVCAAILR	736							
79	11	1898	VVGWCAAILR	737							
93	13	517	VWVGTTDR	738							

Consistency	Frq	Position	Sequence	SeqID Num	Filed	Peptide	A*0301	A*1101	A*3101	A*3301	A*6801
86	12	93	WAGWLLSPR	739							
86	12	96	WLLSPRGSR	740		1 0953	0 0008	0 0005			
100	14	1920	WMNRLIAFASR	741							
79	11	557	WMNSTGFTK	742		1174 16	0 0530	0 0810	0 0014	0 0420	0 0056
93	13	35	YLLPRRGPR	743		1 0951	0 0054	0 0005			
79	11	2930	YSPGEINR	744							
100	14	637	YGGVEIR	745							
86	12	1939	YVPESDAAR	746		1 1065	0 0003	0 0001			

Table X

HCV A24 Super Motif with Binding Information

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*2403
ALLSPGAI	747	1890		8	13	93	
ALAHGPRVI	748	150	1013 16	9	14	100	
ALSTGRIH	749	689	1013 12	9	12	86	
ALVGVVIAAI	750	1896		11	11	79	
ALINLPQSE	751	165		10	13	93	
ALLGIGAY	752	1265		8	14	100	
ALLGFGAYM	753	1265		9	13	93	
AVATYHGI	754	1419		8	14	100	
AVQWNRH	755	1917		8	14	100	
AVQWNRH	756	1917	1174 09	9	14	100	
AVQWNRHAF	757	1917		11	14	100	
AWHMMNRW	758	319		8	12	86	
AVAAAGIKVI	759	1248		10	11	79	0.0009
AVYRLLVSVI	760	1421	13 0132	11	14	100	
CLHKLGVPEL	761	2941	1 0510	10	12	86	
CLWMMILL	762	739		8	12	86	
CLCGSSDL	763	1128		8	11	79	
CLGASSLRY	764	1128	1069 62	9	11	79	
CLCGSSALYL	765	1128		10	11	79	
CLRWAKAVDF	766	1190		11	11	79	
CLWNNSTGF	767	555		9	11	79	
CVTOIVDF	768	1462		8	12	86	
CVTOIVDFSL	769	1462	1 0487	10	12	86	
CYDAGCAW	770	1525		8	11	79	
CLWAGAWI	771	1525	1 0125	9	11	79	
CYDAGCAWTEL	772	1525		11	11	79	
DFSLDPTF	773	1468		8	14	100	
DFSLDPTFH	774	1468		10	14	100	
DLGGSVEL	775	279		8	12	86	
DLEWTSTW	776	1657		9	12	86	
DLEVVISTWVL	777	1657		11	12	86	
DLGVFCEKM	778	2617		10	13	93	
DLMGVPL	779	132		8	11	79	
DLVNLPLAI	780	1883	14 0052	9	11	79	
DLVNLPLAIL	781	1883	1 0891	10	11	79	
DLAAAGDI	782	994		8	12	86	
DLAAGGDI	783	994		9	12	86	
DLTCGFAL	784	124		10	12	86	
DLTCGFADIM	785	124		11	12	86	
DLKFAKGGK	786	21	1174 01	10	12	86	
DYFTRWHG	787	615		9	14	100	
EIPFYGKAI	788	1377	1174 07	9	13	93	
ETAGARLVVL	789	1342		10	12	86	
ETIMRSPVF	790	1207		9	12	86	
EVVISTWVL	791	1659	1 0132	9	12	86	

Sequence	Seq. Id. Num.	Position	Peptide No.	No. of Amino Acids	Sequence Frequency (%)	Conservancy (%)	A*2401
FISGJAVI	792	1773		8	14	100	
FISGJPLAGI	793	1773		11	14	100	
FILALISCI	794	177	10818	9	12	86	
FIFAMTIV	795	1792		8	14	100	
FICLTHIDAF	796	1567		11	13	93	
FILIPALSTCL	797	684		11	11	79	
FWAKRANWF	798	1765	240092	9	12	86	6.9000
FWAKRANWF	799	1765		10	12	86	
GFALIMGY	800	129		8	13	93	
GFALIMGY	801	129		9	13	93	
GFALIMGY	802	129		11	11	79	
GFALIMGY	803	1669		9	11	79	
GFALIMGY	804	1776		8	14	100	
GFALIMGY	805	1776		11	14	100	
GFALIMGY	806	1552	10126	9	13	93	
GFALIMGY	807	1552		11	12	86	
GFALIMGY	808	1921	107303	10	11	79	0.0001
GFALIMGY	809	1782		11	11	79	
GFALIMGY	810	1569		9	13	93	
GFALIMGY	811	1569	10488	10	13	93	
GFALIMGY	812	1963		8	11	79	
GFALIMGY	813	1863		9	12	86	
GFALIMGY	814	1193		8	11	79	
GFALIMGY	815	1670	117419	9	12	86	
GFALIMGY	816	1670		11	12	86	
GFALIMGY	817	161	10099	9	11	79	
GFALIMGY	818	2619		8	14	100	
GFALIMGY	819	2619	10504	10	14	100	
GFALIMGY	820	2619		11	14	100	
GFALIMGY	821	154		11	12	86	
GFALIMGY	822	1900		8	11	79	
GFALIMGY	823	1027		8	11	79	
GFALIMGY	824	1027		11	11	79	
GFALIMGY	825	1859	130133	10	12	86	0.0003
GFALIMGY	826	135	130131	10	11	79	0.0057
GFALIMGY	827	2728		11	12	86	
GFALIMGY	828	696		11	11	79	
GFALIMGY	829	1719		9	11	79	
GFALIMGY	830	1769	117408	9	13	93	
GFALIMGY	831	1769		11	13	93	
GFALIMGY	832	2855		8	12	86	
GFALIMGY	833	2855		11	12	86	
GFALIMGY	834	1910		11	11	79	
GFALIMGY	835	176		10	12	86	
GFALIMGY	836	1816	109016	10	12	86	0.0026

Sequence	Seq'd Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401
ILGILVI	837	1331		8	12	86	
IMAKREVI	838	2591		8	12	86	
ITSTIGAKI	839	1296		9	12	86	
ITSTIGAKI	840	1296		10	11	79	
IVWDYLY	841	701		8	12	86	
IVFVYLI	842	30		8	13	93	
KVYFAA	843	23		8	13	93	
KVYITICF	844	121		10	12	86	
IFNIGAW	845	1813		8	12	86	
IEADLIW	846	2235		8	12	86	
ININRSW	847	414		8	11	79	
ILALSLI	848	178		8	12	86	
ILAPITAY	849	1030		8	14	100	
ILNIGAW	850	1812		9	12	86	
ILPAIISGAL	851	1887		11	13	93	
ILPRRGR	852	36	24 0066	9	13	93	
ILSPRRSRPSW	853	97		11	11	79	
ILWIKMGRNI	854	2240		11	12	86	
ITCGALD	855	126		8	12	86	
ITCGALRM	856	126		9	12	86	
ITCGALRMGY	857	126		11	12	86	
ITIDAHF	858	1570		8	13	93	
ITIDAHFI	859	1570		9	13	93	
ITSMITDPSHF	860	2176		11	13	93	
ITTSCHNII	861	2738		9	11	79	
IVDIAGY	862	1853		8	11	79	
LVGVLAAL	863	1667	1 0133	9	12	86	
LVINPSVAATL	864	1257		11	14	100	
LVNLPAL	865	1884		8	11	79	
LVNLPAIL	866	1884	1 0825	9	11	79	
LVTRHADI	867	1137	14 0048	9	11	79	
LVGVVCAAI	868	1897	40 0141	10	11	79	
LVGVVCAAIL	869	1897		11	11	79	
LWARMIM	870	2872		8	12	86	
LWARMIMTHF	871	2872		11	12	86	
LWARMIMTHF	872	2241		10	12	86	
LWARMIMTHF	873	1135		11	11	79	
LVIVTRHADI	874	2876		8	12	86	
MLMTHFF	875	2179		8	14	100	
MLIDFSHI	876	1770		8	14	100	
MWNIISGL	877	1770		10	14	100	
MWNIISGLGY	878	1770		11	14	100	
MWNIISGLGYL	879	636	1073 18	10	13	93	0 0270
MVVGAVNIFRL	880	1772		8	14	100	
NFSIGGY	881	1772	24 0091	9	14	100	0 0170
NFISGQYL							

Sequence	Seq(S) Then	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401
NIICAWVAAGI	882	1815		11	12	86	
NIHICAVRII	883	1282	1174 06	9	11	79	
NIHIVAGI	884	700		8	12	86	
NIHIVAGIY	885	700	1073 01	9	12	86	0.0001
NIHIVGII	886	318	939 18	9	12	86	
NIHIVRIIM	887	2239		8	12	86	
NIHIVSGSI	888	168	1174 02	9	13	93	
NIHIVSGSI	889	168		10	13	93	
NIHIVSGSI	890	168		11	13	93	
NIHIVSGSI	891	1460		10	12	86	
NIHIVSGSI	892	416		8	13	93	
NIHIVSGSI	893	14		11	11	79	
NIHIVSGSI	894	1108		9	11	79	
NIHIVSGSI	895	551		8	12	86	
NIHIVSGSI	896	1295		10	11	79	
NIHIVSGSI	897	1295		11	11	79	
NIHIVSGSI	898	2403		11	13	93	
NIHIVSGSI	899	143	1 0093	9	11	79	
NIHIVSGSI	900	2667		11	11	79	
NIHIVSGSI	901	109		11	12	86	
NIHIVSGSI	902	1621		9	11	79	
NIHIVSGSI	903	1621		10	11	79	
NIHIVSGSI	904	1621		11	11	79	
NIHIVSGSI	905	2870		8	11	79	
NIHIVSGSI	906	2870		9	11	79	
NIHIVSGSI	907	2870		10	11	79	
NIHIVSGSI	908	1626		8	14	100	
NIHIVSGSI	909	1554		9	12	86	
NIHIVSGSI	910	1554		10	12	86	
NIHIVSGSI	911	2857	1174 13	9	14	100	
NIHIVSGSI	912	2857	1174 14	10	14	100	
NIHIVSGSI	913	2857		11	12	86	
NIHIVSGSI	914	2318		8	11	79	
NIHIVSGSI	915	1732		9	12	86	
NIHIVSGSI	916	1732		10	12	86	
NIHIVSGSI	917	29		8	13	93	
NIHIVSGSI	918	29	1 0088	9	13	93	
NIHIVSGSI	919	1465		11	12	86	
NIHIVSGSI	920	1919		9	14	100	
NIHIVSGSI	921	1778	13 0075	9	14	100	0.0480
NIHIVSGSI	922	2647	13 0134	10	11	79	0.0180
NIHIVSGSI	923	2647		11	11	79	
NIHIVSGSI	924	2918		8	12	86	
NIHIVSGSI	925	2918	1090 21	10	12	79	0.0001
NIHIVSGSI	926	2611		8	11	79	

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A: 0.0041
RLIAPITAY	927	1029	1174 18	9	12	86	
RMADWMM	928	317		8	12	86	
RMADWMMNNW	929	317		10	12	86	
RMIMMTHF	930	2875		8	12	86	
RMIMMTHF	931	2875		9	12	86	
RMVAVNIFRL	932	635		11	13	93	
RVEFKMAL	933	2621		8	14	100	
RVEFKMAL Y	934	2621	1174 21	9	14	100	
RMEFKMAY	935	156	1174 17	9	12	86	
SFSEILAI	936	173		9	14	100	
SFSEILAI I	937	173	24 0108	10	14	100	0.0041
SFSEILAI I	938	175		8	14	100	
SFSEILAI SGI	939	175		11	12	86	
SLDPTFI	940	1470		8	14	100	
SLHSYSPRI	941	2926	1174 15	10	11	79	
SMIDPSYH	942	2178	1174 10	9	14	100	
STKVPAAV	943	1242		8	12	86	
STLPGNPAI	944	1784	40 0083	9	11	79	
STWLVGMI	945	1663		10	12	86	
SVAATIGF	946	1262		8	14	100	
SVAATIGF GAV	947	1262		11	14	100	
SWCKMMWGI	948	1608		9	11	79	
SWLGNIM	949	2860		8	12	86	
SYKGGSGAPL	950	1164		11	12	86	
TIMAKNEVF	951	2590		9	11	79	
TIGFGAYM	952	1266		8	13	93	
TIHGPTFI	953	1622		8	11	79	
TIHGPTFI L	954	1622	1 0129	9	11	79	
TIHGPTILY	955	1622	1073 04	10	11	79	0.0001
TIIFNLGGW	956	1811		10	12	86	
TIIPAI STGL	957	686		9	11	79	
TIIPALSTGI I	958	686	1 0108	10	11	79	
TIIPGNPAI	959	1785	1174 03	8	11	79	
TIICGFADL	960	125	1 0092	9	12	86	
TIICGFADIM	961	125		10	12	86	
TIWARMH	962	2871		8	11	79	
TIWARMH M	963	2871		9	11	79	
TIIMAKNEVF	964	2589		10	11	79	
TIIPAL STGL	965	685		10	11	79	
TIIPALSTGI I	966	685		11	11	79	
TIIPSPVF	967	1208		8	12	86	
TIISGNI L	968	2739		8	11	79	
TIQESLDPTE	969	1466		10	12	86	
TIWMNSTGI	970	556		8	11	79	
TIWLVGSL	971	1664		9	12	86	

ICV A24 Super Motif With Binding Information

Sequence	SeqId Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	Accepted
1 2 3 4 5 6 7	972	1297	13 0074	8	13	93	
1 2 3 4 5 6 7	973	1297		9	12	86	0.0240
1 2 3 4 5 6 7	974	1566		8	13	93	
1 2 3 4 5 6 7	975	1566		9	12	86	
1 2 3 4 5 6 7	976	1671		8	12	86	
1 2 3 4 5 6 7	977	1671	109020	10	12	86	0.0070
1 2 3 4 5 6 7	978	157		8	12	86	
1 2 3 4 5 6 7	979	1258	1 0483	10	14	100	
1 2 3 4 5 6 7	980	2737	1 0505	10	11	79	
1 2 3 4 5 6 7	981	1852		9	11	79	
1 2 3 4 5 6 7	982	1666	1 0492	10	12	86	
1 2 3 4 5 6 7	983	2639		8	11	79	
1 2 3 4 5 6 7	984	2639		10	11	79	
1 2 3 4 5 6 7	985	1463		9	12	86	
1 2 3 4 5 6 7	986	1138		8	11	79	
1 2 3 4 5 6 7	987	1439		8	11	79	
1 2 3 4 5 6 7	988	1898		9	11	79	
1 2 3 4 5 6 7	989	1898		10	11	79	
1 2 3 4 5 6 7	990	1660		8	12	86	
1 2 3 4 5 6 7	991	34	107319	11	13	93	0.0016
1 2 3 4 5 6 7	992	1920		8	14	100	
1 2 3 4 5 6 7	993	1665		8	12	86	
1 2 3 4 5 6 7	994	1665		11	12	86	
1 2 3 4 5 6 7	995	136	1 0817	9	11	79	
1 2 3 4 5 6 7	996	1779		8	14	100	
1 2 3 4 5 6 7	997	1165	1 0479	10	12	86	
1 2 3 4 5 6 7	998	1165		11	12	86	
1 2 3 4 5 6 7	999	35	107307	10	13	93	0.0001
1 2 3 4 5 6 7	1000	1136		10	11	79	
1 2 3 4 5 6 7	1001	1106		8	11	79	
1 2 3 4 5 6 7	1002	1106		11	11	79	
1 2 3 4 5 6 7	1003	276		10	12	86	
1 2 3 4 5 6 7	1004	276		11	12	86	
1 2 3 4 5 6 7	1005	637	1 0107	9	13	93	
1 2 3 4 5 6 7	1006	1422		10	14	100	

Table Xi
ICV B07 Super Motif (with Binding Information)

Conservancy	Freq	Position	Sequence	SeqID Num	Filed	Peptide	R*5702	R*5501	R*5101	R*5301	R*5401
86	12	1604	APPSWDOM	1007		15 0051	0 002R	0 0002	0 0002	0 0001	0 0002
79	11	1604	APPSWDOMW	1008		15 0233	0 0001	0 0001	0 0002	0 0006	0 0003
93	13	1235	APTSGKSTKV	1009		29 0117	0 0001				
79	11	2869	APTLWARM	1010	*	29 0031	0 0031	0 0031	0 0012	0 0002	0 0023
79	11	2869	APTLWARM	1011	*	15 0063	0 0160	0 0002	0 0012	0 0001	0 0002
79	11	2869	APTLWARMIL	1012	*	15 0247	0 8800	0 0001	0 0010	0 0001	0 0003
79	11	2869	APTLWARMILM	1013	*	29 0118	0 0130	0 0001	0 0003	0 0002	0 0033
79	11	2410	DPDLSGSW	1014		15 0058	0 0001	0 0002	0 0002	0 0005	0 0002
86	12	111	DPRRSRNL	1015	*	15 0043	0 0170	0 0002	0 0001	0 0001	0 0002
79	11	2615	FDPLGVRV	1016		29 0032	0 0001				
100	14	24	FPGGGV	1017		29 0033	0 0001				
100	14	24	FPGGGVGV	1018		29 0119	0 0001				
86	12	1912	GPFGAVDM	1019		15 0055	0 0001	0 0032	0 0002	0 0001	0 0002
86	12	1912	GPFGAVDMW	1020		15 0240	0 0001	0 0031	0 0002	0 0001	0 0003
93	13	41	GPRLGVRA	1021		29 0034	0 0001				
100	14	1625	GPTPLLYRL	1022		15 0053	0 0024	0 0032	0 0002	0 0001	0 0002
93	13	1625	GPTPLLYRLGA	1023		29 0120	0 0005				
93	13	507	GPVCFTPSPV	1024		29 0121	0 0001				
93	13	1378	IPFYGKAI	1025	*	29 0035	0 0120	0 0031	0 0002	0 0001	0 0003
79	11	137	IPLVGAPL	1026	*	29 0036	0 4400	0 0032	0 0700	0 0003	0 0035
86	12	2608	KPARLIVF	1027	*	29 0037	0 0150	0 0032	0 0017	0 0002	0 0006
79	11	2608	KPARLIVFPDL	1028		29 0122	0 0003				
79	11	1620	KPTLHGPTPL	1029	*	15 0234	1 4150	0 0031	0 0002	0 0001	0 0003
79	11	1620	KPTLHGPTPL	1030		29 0123	0 0021				
93	13	1888	LPAILSPGA	1031	*	16 0013	0 0001	0 0001	0 0001	0 0002	0 9400
93	13	1888	LPAILSPGAL	1032	*	15 0238	0 0053	0 0001	0 0036	0 0001	0 2100
86	12	1888	LPAILSPGALV	1033		29 0124	0 0003				
100	14	687	LPALSTGL	1034	*	29 0038	0 0020	0 0002	2 0000	0 0062	0 0005
86	12	687	LPALSTGLI	1035		15 0048	0 0350				
86	12	687	LPALSTGLIHL	1036		29 0125	0 0011				
86	12	2165	LPCEPEPDV	1037		15 0056	0 0001	0 0002	0 0001	0 0001	0 0002
93	13	169	LPGCSFSI	1038	*	29 0039	0 0110	0 0360	0 0059	0 0150	0 0016
93	13	169	LPGCSFSIF	1039	*	1145 12	0 1950	0 0796	0 0050	0 0813	0 0015
93	13	169	LPGCSFSIFL	1040	*	15 0220	0 0022	0 0009	0 0100	0 0140	0 0012
93	13	169	LPGCSFSIFLL	1041		29 0126	0 0007				
93	13	37	LPRRGPRL	1042	*	29 0040	6 5000	0 0001	0 0180	-0 0002	0 0020
93	13	37	LPRRGPRLGV	1043	*	15 0218	0 1900	0 0001	0 0009	0 0001	0 0025
93	13	1553	LPVCOOHL	1044	*	29 0041	0 0005	0 0046	0 0002	0 0110	0 0003
86	12	1553	LPVCOOHLF	1045		15 0232	0 0001				
86	12	1553	LPVCOOHLFW	1046		29 0127	0 0001				
86	12	1720	LPVCOOHLFW	1047	*	29 0042	0 0130	0 0001	0 0040	-0 0002	0 0013
100	14	1260	NPSVAATL	1048		29 0043	0 0011				
86	12	1605	NPSVAATLGF	1049		15 0230	0 0001	0 0001	0 0002	0 0001	0 0003
86	12	1605	PPPSWDOM	1050		29 0044	0 0003				
79	11	1605	PPPSWDOMW	1051		15 0052	0 0001	0 0002	0 0001	0 0001	0 0002
79	11	1606	PPSWDOMW	1052		29 0045	0 0002				
79	11	1606	PPSWDOMWKC	1053		29 0128	0 0001				
79	11	2317	PPVW-HGCP	1054	*	1292 17	0 0140	0 0001	0 0001	0 0001	-0 0002
79	11	2601	QPEKGGKPA	1055	*	16 0188	0 0011	0 0001	0 0001	0 0002	0 0190
79	11	2808	QPEYOLE	1056		29 0046	0 0002				
79	11	2808	QPEYOLEU	1057		15 0062	0 0001	0 0002	0 0002	0 0001	0 0002
86	12	78	QPGYPAWPL	1058		29 0047	0 0006				

Conservancy	Freq	Position	Sequence	SeqID Num	Filed	Peptide	B*0702	R*3501	R*5101	R*5301	R*5401
86	12	78	QPGYPMPLY	1059		15 0040	0 0001	0 0011	0 0002	0 0001	0 0002
93	13	57	QPRGRRCPI	1060	.	15 0039	0 2300	0 0002	0 0001	0 0001	0 0002
79	11	2299	RPDYNPL	1061		29 0048	0 0050				
93	13	1893	SPGALVGV	1062	.	15 0054	0 0001	0 0002	0 0002	0 1200	0 0002
79	11	1893	SPGALVGV	1063	.	15 0239	0 0130	0 0001	0 0016	0 0001	0 0003
79	11	2931	SPGEINRV	1064		29 0049	0 0007				
79	11	2931	SPGEINRV	1065		16 0015	0 0003	0 0001	0 0001	0 0002	0 0037
79	11	2649	SPGQRMVF	1066		29 0050	0 0027				
79	11	2649	SPGQRMVF	1067	.	15 0060	0 1200	0 0002	0 0002	0 0001	0 0002
79	11	99	SPRGRPSW	1068	.	15 0042	0 3800	0 0002	0 0005	0 0001	0 0002
86	12	1935	SPTHYVPESDA	1069		29 0129	0 0001				
86	12	1975	TPCGSWL	1070		29 0051	0 0028	0 0001	0 0002	0 0001	0 0003
79	11	1126	TPCTCGSSDL	1071		15 0228	0 0005				
79	11	1126	TPCTCGSSDL	1072		29 0130	0 0001				
86	12	223	TPGCVPCV	1073		29 0052	0 0001				
93	13	1550	TPGLPVODHL	1074		29 0131	0 0001				
93	13	1627	TPILYRLGA	1075	.	16 0017	0 0083	0 0001	0 0001	0 0002	0 2300
93	13	1627	TPILYRLGAV	1076	.	15 0235	0 0120	0 0001	0 0008	0 0001	0 0110
86	12	2856	TPVNSWLGNI	1077		15 0246	0 0001	0 0001	0 0053	0 0006	0 0003
86	12	2856	TPVNSWLGNI	1078		29 0132	0 0001				
86	12	1940	VPESDAAA	1079		29 0053	0 0022				
86	12	1940	VPESDAAARV	1080		15 0241	0 0001	0 0001	0 0010	0 0001	0 0003
86	12	799	WPLLLLL	1081		29 0054	0 0021				
100	14	616	YPYRLWHY	1082		29 0055	0 0001				

Table XII

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Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
AKHAWNFI	1083	1767		8	12	86
AKIEVFCV	1084	2593		8	12	86
AFALAHGV	1085	148		8	14	100
DHCELSFL	1086	663		8	11	79
EKGGRKPA	1087	2603		8	11	79
EKMALYDV	1088	2624		8	12	86
EKKALCL	1089	1733		8	12	86
GHRMAWDM	1090	315		8	13	93
GKSIKVA	1091	1240		8	12	86
GKPARLI	1092	2606		8	11	79
HRMAWDM	1093	316		8	13	93
IKGGRRL	1094	1390		8	11	79
IHTGVRTI	1095	1283		8	11	79
KKCDELA	1096	1403		8	14	100
KKCDELA	1097	1402		8	14	100
LIIGPTLL	1098	1623		8	11	79
IKKNDV	1099	697		8	12	86
LIOLAVAV	1100	969		8	11	79
NIIVSPHY	1101	1932		8	12	86
PIGRKQPI	1102	58		8	13	93
PIGRKQPI	1103	100		8	11	79
PIGRKQPI	1104	112		8	12	86
PIGRKQPI	1105	1140		8	11	79
PIGRKQPI	1106	2854		8	12	86
PIGRKQPI	1107	2943		8	12	86
PIGRKQPI	1108	2607		8	11	79
PIGRKQPI	1109	2730		8	13	93
PIGRKQPI	1110	39		8	13	93
PIGRKQPI	1111	17		8	12	86
PIGRKQPI	1112	1401		8	14	100
PIGRKQPI	1113	116		8	12	86
PIGRKQPI	1114	1571		8	13	93
PIGRKQPI	1115	2985		8	12	86
PIGRKQPI	1116	1243		8	12	86
PIGRKQPI	1117	2674		8	14	100
PIGRKQPI	1118	1191		8	11	79
PIGRKQPI	1119	2620		8	14	100
PIGRKQPI	1120	155		8	13	93
PIGRKQPI	1121	1423		8	14	100
PIGRKQPI	1122	2853		9	11	79
PIGRKQPI	1123	2610		9	11	79
PIGRKQPI	1124	1346		9	11	79
PIGRKQPI	1125	2874		9	12	86
PIGRKQPI	1126	2298		9	11	79
PIGRKQPI	1127	663		9	11	79

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
EKMAL YUVV	1128	2624		9	12	86
EKGJAL GLL	1129	1733		9	12	86
GHRMAWIMMM	1130	315		9	13	93
GKSTKVPAA	1131	1240		9	12	86
GRRPARIV	1132	2606		9	11	79
HRMAWIMMM	1133	316		9	12	86
IKGGRHIF	1134	1390		9	11	79
IKKGLHFLAA	1135	1402		9	14	100
IKGLSARSL	1136	2919		9	11	79
IKGPHTLY	1137	1623		9	11	79
IKSSSGRI	1138	2927		9	11	79
IKSSSGRI	1139	1166		9	12	86
IKKLGARFI	1140	2942		9	12	86
IKVSETHYV	1141	1932		9	12	86
IKRRLVKKI	1142	16		9	11	79
IKRRRLGV	1143	38		9	13	93
IKRPVNSWL	1144	2854		9	12	86
IKMPCYFCA	1145	1909		9	11	79
IKPARIIV	1146	2607		9	11	79
IKRIRASGL	1147	2739		9	12	86
IKSRRLGRV	1148	114		9	12	86
IKRRRLHIA	1149	1401		9	14	100
IKVVFESIA	1150	1937		9	12	86
IKVPAAYAA	1151	1243		9	11	79
IKHADVIV	1152	1139		9	11	79
IKVSEIRKV	1153	2251		9	12	86
IKRPGYGL	1154	22		9	13	93
IKVCEKML	1155	2620		9	14	100
IKRLAPITA	1156	1028		9	11	79
IKRIMLJFI	1157	2242		9	12	86
IKGLDVSVI	1158	1423		9	14	100
IKRIRASGL	1159	2729		9	13	93
IKRALHGVIV	1160	148		10	14	100
IKRAQPFVSW	1161	1600		10	11	79
IKHIFVNSWL	1162	2853		10	11	79
IKMILMTHFI	1163	2874		10	12	86
IKSRRLCTEL	1164	1399		10	14	100
IKRRLSPIL	1165	661		10	11	79
IKRRLSPIL	1166	663		10	11	79
IKGIRPARL	1167	2603		10	11	79
IKRAVCIRGV	1168	1185		10	12	86
GHRMAWIMMM	1169	315		10	12	86
GKSTKVPAA	1170	1240	24 0036	10	12	86
GRRPARIV	1171	2606		10	11	79
KHAWRIISFI	1172	1768		10	13	93

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)
KKKLEIAAKK	1173	1403		10	12	86
LEKQIMVJY	1174	697		10	11	79
LEKQVAFLL	1175	1166		10	12	86
QKALALQTA	1176	1735		10	12	86
RRWAFKAV	1177	1909		10	11	79
RRWAFKAVRA	1178	39		10	13	93
RRWAFKCA	1179	1908		10	11	79
RRWAFKVK	1180	113		10	12	86
RRWAFKVKI	1181	114		10	12	86
SKGGGAKDV	1182	2552		10	12	86
SKKKLHAA	1183	1401		10	14	100
THVVFSLQAA	1184	1937		10	12	86
THVYAKAVDF	1185	1191		10	11	79
THVYSEKRV	1186	2251		10	12	86
VKIPKAFKAV	1187	22		10	13	93
VHVFELKALY	1188	2620		10	14	100
VHVFELKALY	1189	155		10	12	86
VHVFELKALY	1190	1028		10	11	79
YKVIKIPKSV	1191	1254		10	14	100
YKVIKIPKSV	1192	2729		10	12	86
YKVIKIPKSV	1193	152		11	13	93
AKGVHVFELKSV	1194	1767		11	12	86
AKHMMVFESGI	1195	148		11	14	100
ARALAKGVRL	1196	2610		11	11	79
ARALAKGVRL	1197	1399		11	14	100
CHSKKKLELA	1198	661		11	11	79
DEKRSLSPL	1199	2603		11	11	79
EKGGRFAPRL	1200	1185		11	11	79
FRAAVCIRGVA	1201	1240		11	12	86
GKSTRVFAAFA	1202	120		11	12	86
GKVIDHLAGF	1203	316		11	12	86
HMMAMMMNNW	1204	1402		11	12	86
KKKLEIAAKL	1205	12		11	12	86
KNNINRFQDV	1206	1623		11	11	79
LHGPTFLYRL	1207	697		11	11	79
LHNNIMVQEL	1208	1619		11	11	79
LKPTLHGPFL	1209	1907		11	11	79
LRWAFKFCGA	1210	38		11	13	93
PERGFELKAVRA	1211	112		11	12	86
PERGFELKAV	1212	1908		11	11	79
RRWAFKAV	1213	113		11	12	86
RKRSNIGKVI	1214	1929		11	12	86
SRGGRVSPHY	1215	116		11	12	86
SRNCKVDTL	1216	1937		11	12	86
THVVFSLQAAA	1217	155		11	12	86
VHVFELKALY						

Sequence	Calculated	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
YKVI VITP/NA	1218	1253		11	14	100

Table XIII

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Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)
AAILRHIV	1219	1904		8	13	93
AALAAVCL	1220	1673		8	12	86
AALGYKVL	1221	1250		8	11	79
AAILGFCA	1222	1264		8	14	100
AAVCTRGV	1223	1187		8	12	86
ASIMAFIA	1224	1793		8	11	79
ASSASOL	1225	2204		8	14	100
ATLGFQAY	1226	1265		8	14	100
CSFSIFLL	1227	172		8	14	100
CSGGAYDI	1228	1310		8	12	86
CSNVSVVA	1229	2819		8	14	100
CICGSSQL	1230	1128		8	11	79
CIRGVAKA	1231	1190		8	11	79
DTAACGDI	1232	934		8	12	86
DILTCGFA	1233	124		8	12	86
EALENLV	1234	750		8	11	79
FAMIRYSA	1235	2794		8	14	100
ESDAARV	1236	1942		8	12	86
ETAGARLV	1237	1342		8	12	86
ETIMRSPV	1238	1207		8	12	86
FADLMGYI	1239	130		8	13	93
FASQKNHV	1240	1927		8	14	100
FSIFLLAL	1241	174		8	14	100
FSYDTRCF	1242	2670		8	11	79
FTEAMTRY	1243	2792		8	14	100
FIPSPWV	1244	512		8	13	93
GAGVAGAL	1245	1861		8	12	86
GAHWGVLA	1246	350		8	12	86
GALWGWV	1247	1895		8	11	79
GARLVLA	1248	1345		8	12	86
GSGKSTKV	1249	1238		8	13	93
GSSDLVLA	1250	1131		8	12	86
GSSGGRL	1251	1168		8	12	86
GSSYGFOY	1252	2641		8	11	79
GIFPINAY	1253	2063		8	11	79
HSYSFGEI	1254	2928		8	11	79
HIIPNSWL	1255	2855		8	12	86
ISGIOYLA	1256	1774		8	14	100
ITSCSSNV	1257	2816		8	14	100
IHWGADTA	1258	989		8	12	86
KSTKVPAA	1259	1241		8	12	86
LAGYGAGV	1260	1857		8	11	79
LAHGRVL	1261	151		8	14	100
LAVAVEPV	1262	972		8	11	79
LSAPSLKA	1263	2211		8	11	79

Sequence	SeqB Motif	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
LSHAAVV	1264	1892		8	13	93
LSHAIH	1265	690		8	12	86
LCGFAH	1266	126		8	12	86
LEHAE	1267	1570		8	13	93
MSAEVV	1268	1654		8	11	79
FWGPH	1269	2859		8	14	100
HCVIV	1270	1460		8	12	86
NINFWH	1271	416		8	13	93
FAISFA	1272	1889		8	13	93
PAISTH	1273	688		8	12	86
PLWAKH	1274	2870		8	11	79
PELVH	1275	1626		8	14	100
QAVV AHA	1276	1595		8	13	93
HARFWM	1277	3019		8	14	100
RSLSH	1278	664		8	11	79
RSRLGH	1279	115		8	12	86
SASLHSH	1280	2923		8	11	79
SSASGHA	1281	2206		8	14	100
STKVPAA	1282	1242		8	12	86
STLPRHA	1283	1784		8	14	100
STLFQAM	1284	2633		8	12	86
STYKHA	1285	1299		8	12	86
TACGHI	1286	995		8	12	86
IAGALVV	1287	1343		8	12	86
TMRSPI	1288	1208		8	12	86
ITSGNH	1289	2739		8	11	79
VAGALVA	1290	1864		8	12	86
VIRHADI	1291	1138		8	11	79
VTSIWWV	1292	1661		8	12	86
WAKHWNF	1293	1766		8	12	86
WAKVIVM	1294	368		8	14	100
WADVGVW	1295	76		8	12	86
YAAJYKV	1296	1249		8	11	79
YSIFPLH	1297	2905		8	11	79
YSTGKFI	1298	1298		8	12	86
YINVKH	1299	1106		8	11	79
AAKLDKTM	1300	2758		9	16	114
AAGYKVI	1301	1250		9	11	79
AARALHGV	1302	147		9	11	79
AATLGFAY	1303	1264		9	14	100
AAVCTHWA	1304	1187		9	11	79
ASDLSAFSL	1305	2208		9	13	93
ATLFGAYM	1306	1265		9	26	186
ATVCAHQA	1307	1596		9	11	79
CAAILRHV	1308	1903		9	13	93

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)
CAWVELTPA	1309	1530		9	11	79
CSISFLLA	1310	172		9	14	100
CSGAYDII	1311	1310		9	12	86
CIGGSSIIY	1312	1128	1 0118	9	11	79
CHGVAKAV	1313	1190		9	11	79
CWNNSTGF	1314	555		9	11	79
DACAWVEL	1315	1527		9	11	79
DTAACGDI	1316	994		9	12	86
DHCTLSIV	1317	2673		9	13	93
ETAGARVV	1318	1342		9	12	86
FTMRSPVF	1319	1207		9	12	86
FSFLLAL	1320	174		9	14	100
FSLDPTII	1321	1469		9	14	100
FGLTHDA	1322	1567		9	13	93
GAGVAGALV	1323	1861		9	12	86
GALVAIKIM	1324	1866		9	12	86
GALVAFKVM	1325	1866		9	14	100
GAVDMMRIL	1326	1916	24 0061	9	14	100
HSPKPDIL	1327	1400		9	14	100
HIFGVKPV	1328	222		9	11	79
ITWGAUTAA	1329	989		9	12	86
ITVSTIRKF	1330	1296		9	12	86
KALGLIOTA	1331	1736		9	12	86
KSTKVPAAV	1332	1241		9	12	86
LAALAAICLL	1333	1672	13 0016 24 0068	9	12	86
LAEDFKKA	1334	1729		9	12	86
LAGLAYYSM	1335	356		9	14	100
LAGYGAGVA	1336	1857		9	11	79
LSAFSLHSY	1337	2922		9	11	79
LSTLGNPA	1338	1783	13 0019	9	14	100
LTCGFADLM	1339	126		9	24	171
LTDPSHITA	1340	2180		9	14	100
ITGRKIQV	1341	1952		9	12	86
ITHDHFTL	1342	1570		9	13	93
ITISGNIIL	1343	2738		9	11	79
MAPLEVFVV	1344	2592		9	12	86
MAWIMMMNW	1345	318	24 0069	9	13	93
NAVATYRGL	1346	1418		9	12	86
NSLRRHIM	1347	2481		9	13	93
NSWLGNIM	1348	2859		9	14	100
NINRRQOV	1349	14		9	24	171
PAILSPGAI	1350	1889		9	12	86
PSVAATLGF	1351	1261		9	13	93
PTLHGPIPL	1352	1621		9	14	100
PTLWAFMIL	1353	2870		9	11	79

Sequence	SeqID:Rum	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservativ (%)
OAE LAARH	1354	1340		9	12	86
RAAVLIRGV	1355	1386		9	12	86
RAIAIRVRV	1356	149	24 0063	9	14	100
RACALPPSW	1357	1601		9	11	79
RAYAMIRRM	1358	811		9	16	114
RSLLSRIIL	1359	664		9	11	79
RSPRIKRI	1360	115		9	12	86
SSASQISA	1361	2205		9	14	100
STKVPAAVA	1362	1242		9	12	86
SLIPGRIAI	1363	1784	40 0083	9	11	79
SIWLVIRGV	1364	1663		9	12	86
TAGARI VVI	1365	1343		9	12	86
TSCSNVSV	1366	2817		9	14	100
TIMAKRI V	1367	2589		9	11	79
VAATLGRGA	1368	1263		9	14	100
VAGGIRVGM	1369	933		9	14	100
VATGATVCA	1370	1592	40 0071	9	12	86
VATIRRIIV	1371	1420	24 0064	9	14	100
VSIILPAVM	1372	2632		9	12	86
VITQVIRSI	1373	1463		9	12	86
WAKHWNFI	1374	1766	24 0070	9	12	86
YAAQGRVLI	1375	1249		9	11	79
YAPTIWARM	1376	2868		9	14	100
YSPCFIRIV	1377	2930		9	11	79
YSPGIRNFI	1378	2648		9	11	79
YSTIGKILA	1379	1298		9	12	86
YTNVCKIV	1380	1106		9	11	79
YAAQGRVVI	1381	1250		10	11	79
AATLGFQAYM	1382	1264		10	26	186
ASLRVFTEAM	1383	2787		10	12	86
ASSASQISA	1384	2204		10	14	100
ATGNLPGSF	1385	165		10	13	93
CSFSIFLLAL	1386	172		10	14	100
CIGGSSRLTL	1387	1128		10	11	79
DARVCACIWM	1388	733		10	18	129
DSMDNICY	1389	1454		10	12	86
DILTCGRAL	1390	124		10	12	86
ENILWRXIM	1391	2237		10	24	171
ETAGARVVI	1392	1342		10	12	86
FADIMGYPI	1393	130		10	11	79
FTEAMIRYA	1394	2792		10	14	100
GAHAALIRGV	1395	146		10	11	79
GADTAACGDI	1396	992		10	12	86
GAGVAGALVA	1397	1861		10	12	86
GALVGVVCA	1398	1895		10	11	79

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)
GAHVVVATA	1399	1345		10	11	79
GAQVMMRRL	1400	1916		10	14	100
GSJKSLKVFPA	1401	1238		10	12	86
GVLEDAFPA	1402	1335		10	14	100
HSKKKQLHA	1403	1400		10	14	100
IAFASTRGRIV	1404	1925		10	14	100
ISGQYLAGL	1405	1774		10	14	100
IRVLSFRKV	1406	2250		10	12	86
ITSSSNVSV	1407	2816		10	14	100
IYSLYGRFL	1408	1296		10	11	79
KSLKVFAYAA	1409	1241		10	12	86
LAKGRSLGA	1410	1305		10	11	79
LAFQIKQKAL	1411	1729		10	12	86
LALPRAYAM	1412	806		10	12	86
LSFGALVVGV	1413	1892		10	13	93
LSPRSRPSW	1414	98		10	11	79
LSRAPRRWF	1415	3017		10	14	100
LSLPLGNPAI	1416	1783		10	11	79
LHPITKYM	1417	1642		10	16	114
NIQVIGTDF	1418	1460		10	12	86
PAISFGALV	1419	1889		10	12	86
PAISGLIHL	1420	688		10	12	86
PARIVFPDL	1421	2609		10	11	79
PSWDMKKCL	1422	1607		10	11	79
PTGSGNSTAV	1423	1236		10	13	93
PTHVVFSDA	1424	1936		10	12	86
PTLHGPIPL	1425	1621		10	11	79
PTLWARMILM	1426	2870		10	22	157
PTPLLRIGA	1427	1626		10	13	93
QAEIAGARLV	1428	1340		10	12	86
QAPPSWDJM	1429	1603		10	24	171
QATVCARAOA	1430	1595		10	11	79
RAAKLODCIM	1431	2757		10	16	114
RAAVCTHGA	1432	1186		10	11	79
RAAHGVRVL	1433	149		10	14	100
SASQISAPSL	1434	2207		10	13	93
SLKVFPAFAA	1435	1242		10	11	79
SLWLVGSL	1436	1663		10	12	86
TAGARLVVLA	1437	1343		10	12	86
TARHFPVNSW	1438	2852		10	11	79
TSSSNVSWA	1439	2817		10	14	100
TSMLEDFSHI	1440	2177		10	13	93
TSMWLVGGV	1441	1662		10	12	86
TTIMAKNEVF	1442	2589		10	11	79
TTIPALSTGL	1443	685		10	11	79

Sequence	Length (aa)	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
VAAITGAG	1444	1263		10	14	100
VIFGFGSGM	1445	1507		10	16	114
VIFGAGVAV	1446	1138		10	11	79
WAGGFWPT	1447	76		10	12	86
WARRMTHF	1448	2873		10	12	86
WARRFWPT	1449	2297		10	11	79
YAGGKVLV	1450	1249		10	11	79
YSGGIRVA	1451	2930		10	11	79
YSGGFWFL	1452	2648		10	11	79
AAHAIAGVRV	1453	147		11	11	79
AAELHVEHAM	1454	2786		11	12	86
AAVITHGAKA	1455	1187		11	11	79
ASGHPVQAM	1456	1717		11	14	100
ASQISAPSLKA	1457	2208		11	11	79
CARAGAPPSW	1458	1599		11	11	79
CSISSEILAL	1459	172		11	14	100
CTGSSILYV	1460	1128		11	11	79
CTRGVAKAVDF	1461	1190		11	11	79
DARVACIWMW	1462	733		11	16	114
DHICGALIM	1463	124		11	24	171
ETAGALVLA	1464	1342		11	12	86
FALHMGYPLV	1465	130		11	11	79
FSHSYSPGET	1466	2925		11	11	79
FTCLTHDAHF	1467	1567		11	13	93
FTLPAISLIL	1468	684		11	11	79
GAUTACGLII	1469	992		11	12	86
GAGVAGALVAF	1470	1861		11	12	86
GALVVGVCAA	1471	1895		11	11	79
GAVOMNRLIA	1472	1916		11	14	100
GSLSKVVVAA	1473	1248		11	12	86
HSKPKDEIAA	1474	1400		11	14	100
HSYSPGFNRV	1475	2928		11	11	79
HFNVFWLGNF	1476	2855		11	12	86
IIRVSEFKVV	1477	2250		11	12	86
IIFGSSNVSA	1478	2816		11	14	100
IYSTGKFLA	1479	1296		11	11	79
KSTKVPAAVAA	1480	1241		11	11	79
LAKKSGGAY	1481	1305		11	11	79
LAGYGAGAGA	1482	1857		11	11	79
LSNLSLPRFHM	1483	2479		11	14	100
LSPGALVGVV	1484	1892		11	11	79
LTCGADMGY	1485	126		11	12	86
LISMIDPSHI	1486	2176		11	13	93
NAVATIRGLDV	1487	1418		11	13	93
NINRFPQVKE	1488	14		11	11	79

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)
PAIATGALVV	1489	1889		11	12	86
PSVAATIGLGA	1490	1261		11	14	100
PIIIRRRRRRI	1491	109		11	12	86
PIIIVPPLGAA	1492	1936		11	12	86
PIIIRRRRIIV	1493	1621		11	11	79
PIIIVPPLGAV	1494	1626		11	13	93
QALTAGALVV	1495	1340		11	12	86
QAPPSMVKMW	1496	1603		11	11	79
QIMRSLPTE	1497	1465		11	12	86
RRRRRRRRRI	1498	55		11	13	93
SAIIEVVSLIW	1499	1655		11	11	79
SSASRRSAPRI	1500	2206		11	13	93
SSIVIVIRRA	1501	1132		11	12	86
SIWIVVAVIA	1502	1663		11	12	86
TARRHPVPSWI	1503	2852		11	11	79
TSIIGRRRRIV	1504	1050		11	12	86
TSIWWVGVVI	1505	1662		11	12	86
TLIPALSLRII	1506	685		11	11	79
VAATIGGAYM	1507	1263		11	26	186
VAGALVAIKVM	1508	1864		11	14	100
VAVI PVVLSIM	1509	974		11	12	86
VAYDALVIGRA	1510	1592		11	11	79
VAYTRILIVSV	1511	1420		11	14	100
VTSIWMVGVV	1512	1661		11	12	86
WAQPGYVWPIY	1513	76		11	12	86
WARMIMTHIF	1514	2873		11	12	86
YAAQGVKVLVI	1515	1249		11	11	79
YATGNIPGCSF	1516	164		11	12	86
YINVCXKLVGVW	1517	1106		11	11	79

Table XIV

HCV B62 Super Motif

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)
AILSPGAL	1518	1890		8	13	93
ALAHGVRV	1519	150		8	14	100
ALGILQTA	1520	1737		8	12	86
APTLWARH	1521	2869	29 0031	8	11	79
AOAPPPSW	1522	1602		8	12	86
ACKYRLV	1523	1251		8	11	79
AVAYYRGL	1524	1419		8	14	100
AVCTRGVA	1525	1188		8	11	79
AVQWMNHL	1526	1917		8	14	100
CLWMMLLI	1527	739		8	12	86
CMSAXLEV	1528	1653		8	11	79
CLXHLFPW	1529	1556		8	12	86
CVTIQVDF	1530	1462		8	12	86
DLIAGTGA	1531	1855		8	12	86
IXGGSVEL	1532	279		8	12	86
DLMGYIPL	1533	132		8	11	79
DLVNLIPA	1534	1883		8	11	79
DJAEATAGA	1535	1339		8	12	86
EIPFYGKA	1536	1377		8	13	93
EUFKQKAL	1537	1731		8	12	86
EVVTSIWV	1538	1659		8	12	86
FISQIYTL	1539	1773		8	14	100
FDKGVRRV	1540	2615	29 0032	8	11	79
FDGGLLV	1541	24	29 0033	8	14	100
FOVAHIIHA	1542	1228		8	12	86
GIQYLAL	1543	1776		8	14	100
GLRLAVA	1544	968		8	11	79
GFRLGVRA	1545	41	29 0034	8	13	93
GVVGLGVY	1546	28		8	14	100
GVAGALVA	1547	1863		8	12	86
GVAKAVDF	1548	1193		8	11	79
GVLAALAA	1549	1670		8	12	86
GVRCERKM	1550	2619		8	14	100
GVVCAAIL	1551	1900		8	11	79
FMGRCEGA	1552	1910		8	11	79
HVSPHIVV	1553	1933		8	12	86
ILGGWVAA	1554	1816		8	12	86
ILGIGIVL	1555	1331		8	12	86
ILSPGALV	1556	1891		8	13	93
IMAKNEVF	1557	2591		8	12	86
IPFYGKAI	1558	1378	29 0035	8	13	93
IPLVGAPL	1559	137	29 0036	8	11	79
INDVQVLY	1560	701		8	12	86
IVFDLGV	1561	2613		8	11	79
IVGGVYIL	1562	30		8	13	93

Sequence	Weight	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
KMALVDDV	1563	2625	29 0037	8	12	86
KCAHIVH	1564	2608		8	12	86
KCKALILL	1565	1734		8	12	86
KVFAAVAA	1566	1244		8	11	79
LHARLW	1567	2235	414	8	12	86
LRTDQW	1568	414		8	11	79
LALISL	1569	178		8	12	86
LALITAY	1570	1030		8	14	100
LILADIV	1571	729	1629	8	13	93
LIVRIGAV	1572	1629		8	13	93
LMGRIIV	1573	133		8	11	79
LPAISLH	1574	687		8	14	100
IFGFSH	1575	169	29 0038	8	13	93
IFRRRHR	1576	37	29 0039	8	13	93
IFVGRH	1577	1553	29 0040	8	13	93
IFVGRH	1578	1720	29 0041	8	13	93
IQDQIMV	1579	2761	29 0042	8	12	86
IVAYQATV	1580	1591	1853	8	12	86
IVDILAGY	1581	1853		8	11	79
IVGMLAA	1582	1667		8	12	86
IVINPSVA	1583	1257		8	14	100
IVNLIPI	1584	1884	1137	8	11	79
IVIRHADV	1585	1137		8	12	86
IVGVVCA	1586	1897		8	11	79
IVVETSA	1587	2773		8	12	86
MLMIRF	1588	2876	2179	8	14	100
MLIDPSH	1589	2179		8	12	86
MLGGWA	1590	1815		8	12	86
NIVIMQYL	1591	700		8	12	86
NLIWPRM	1592	2239	143	8	12	86
NPSVAATH	1593	1260		8	14	100
PLGGAARA	1594	143		8	11	79
PLLYHGA	1595	1628		8	13	93
FPTSWDXM	1596	1605	29 0044	8	12	86
FPSWIKMW	1597	1606	29 0045	8	11	79
FVHGRH	1598	2318	29	8	11	79
QVGRVYL	1599	29		8	13	93
QLIRFJA	1600	336		8	12	86
QRYRHL	1601	2808		8	11	79
QPSYFMT	1602	78	29 0047	8	12	86
RIHNSAF	1603	2918	2611	8	12	86
RIVFDL	1604	2611		8	11	79
RIAPITA	1605	1029		8	12	86
RIVILATA	1606	1347		8	12	86
RIAWQMM	1607	317		8	12	86

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)
IRMLMTHF	1608	2875	29 0048	8	12	86
IRDYHFFI	1609	2299		8	11	79
IRXMXZSJ	1610	2243		8	12	86
IRGFKKAI	1611	2621		8	14	100
IRFSGHKV	1612	2252	29 0049	8	12	86
IRGdHIV	1613	2100		8	11	79
IRILLALI	1614	175		8	14	100
IRIPRIL	1615	1470		8	14	100
IRRFRIV	1616	2931	29 0050	8	11	79
IRXKRF	1617	2649		8	11	79
IRLSAPSL	1618	2209		8	13	93
IRVAAHGF	1619	1262		8	14	100
IRMAKRV	1620	2590	29 0051	8	11	79
IRGCAVM	1621	1266		8	13	93
IRHGFPI	1622	1622		8	11	79
IRFGNFI	1623	1785		8	11	79
IRWAGMII	1624	2871	29 0052	8	11	79
IRCSQSWI	1625	1975		8	12	86
IRGVVIV	1626	273		8	12	86
IRIVHSL	1627	1464		8	12	86
IRCAHADA	1628	1597	29 0053	8	11	79
IRDNFIV	1629	1456		8	12	86
IRAAIAAY	1630	1671		8	12	86
IRGLCYDA	1631	1521		8	13	93
IRNDJALIA	1632	1337	29 0054	8	14	100
IRFGNNY	1633	157		8	12	86
IRNPSVAA	1634	1258		8	14	100
IRVGVVIA	1635	1666		8	12	86
IRVNFVS	1636	1256	29 0055	8	14	100
IRVSSYGF	1637	2639		8	11	79
IRPSDAAA	1638	1940		8	12	86
IRVNNRIL	1639	1918		8	14	100
IRVATDALM	1640	1439	29 0056	8	11	79
IRVGVVIAA	1641	1898		8	12	86
IRVISTWVL	1642	1660		8	14	100
IRVNRILAF	1643	1920		8	14	100
IRVITLIL	1644	799	29 0057	8	12	86
IRVIVRNI	1645	1665		8	12	86
IRVAGLSII	1646	1779		8	14	100
IRVTRWHI	1647	616		8	14	100
IRVPSIDAA	1648	1939	24 0067	8	12	86
IRISGALV	1649	1890		9	12	86
IRVAGVRI	1650	150		9	14	100
IRSTGLHII	1651	689		9	12	86
IRVGVVIA	1652	1896	40 0089	9	11	79

Sequence	ScalfD Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
APFPGWIKAM	1654	1604	15 0051	9	12	86
APFLWARM	1654	2869	15 0063	9	11	79
AGGKQVVI	1655	1551		9	11	79
AGSSTWFL	1656	77		9	12	86
AGVWNRRL	1657	1917	1174 09	9	14	100
CMGALFVV	1658	1653	1 0131	9	11	79
DECSQFLV	1659	279	1 0101	9	11	79
DEVVISTW	1660	1657		9	12	86
DMGYFLV	1661	132	1 0816	9	11	79
DVRLLEAI	1662	1883	14 0052	9	11	79
DVWLEESA	1663	2772		9	11	79
DYLVIRGA	1664	1134	24 0074	9	12	86
ETRLSQSW	1665	2410	15 0058	9	11	79
ETRRSRRL	1666	111	15 0043	9	12	86
ETSYKAI	1667	1377	1174 07	9	13	93
FMGRITRV	1668	2245		9	12	86
FVVISWVI	1669	1659	1 0132	9	12	86
FESIQYLA	1670	1773	40 0082	9	14	100
FLALISCL	1671	177	1 0818	9	12	86
FLITADRV	1672	728	1 0113	9	13	93
FQSPKRW	1673	2646		9	11	79
GGTMDXA	1674	1333		9	14	100
GLPWQRR	1675	1552	1 0126	9	13	93
GLRQAVAV	1676	968	1 0114	9	11	79
GLTHDAIE	1677	1569		9	13	93
GPTFGVWV	1678	1912	15 0055	9	12	86
GPTPLVRI	1679	1625	15 0053	9	14	100
GWGQVRL	1680	28		9	13	93
GVASALVAF	1681	1863		9	12	86
GVLAAALAY	1682	1670	1 0134	9	12	86
GVYATGNI	1683	161	1 0099	9	11	79
GVWTEKMA	1684	2619		9	14	100
GVRMLEXV	1685	154	1 0095	9	13	93
HHQRNIDV	1686	696	1 0111	9	12	86
HLPMELAM	1687	1719		9	11	79
HMWFESEI	1688	1769	1174 08	9	13	93
HRWVWQY	1689	698		9	11	79
HMFEFGAV	1690	1910		9	11	79
ILAGYAGV	1691	1856	1 0135	9	11	79
ILSPGALVV	1692	1891	24 0065	9	13	93
KVILNFSV	1693	1255	1174 05	9	14	100
LITSCSSNV	1694	2815	1 0147	9	14	100
LWFDLGV	1695	2612	1 0826	9	11	79
LILLADA	1696	726	24 0071	9	14	100
LILNLGSW	1697	1812		9	12	86

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (...)
LIHRRJFA	1698	36	24 0066	9	13	93
LPAISFGA	1699	1888	16 0013	9	13	93
LPAISFGI	1700	687	15 0048	9	12	86
LPFIFFTW	1701	2165	15 0056	9	12	86
LPFIFSHF	1702	169	15 0044	9	13	93
LPGAVAAI	1703	1667	1 0133	9	12	86
LVINPSVAA	1704	1257	1 0825	9	14	100
LVRILFAI	1705	1884	14 0048	9	11	79
LVIHIAIVI	1706	1137		9	11	79
LWGVVCAA	1707	1897		9	11	79
NHGGWVAA	1708	1815		9	12	86
NHRTGVRH	1709	1282	1174 06	9	11	79
NVWVDFY	1710	700	1 0112	9	12	86
NIGKVHDI	1711	118	1 0091	9	12	86
NIPYCSLS	1712	168	1174 02	9	13	93
NMCKXVW	1713	1108		9	11	79
PIGGAAAI	1714	143	1 0093	9	11	79
PLVYRGAV	1715	1628	1 0130	9	13	93
PPSSWIXXW	1716	1605	15 0052	9	11	79
PPVVRJFV	1717	2317	29 0070	9	11	79
PXFFVHFI	1718	2807		9	11	79
PVXXHLEI	1719	1554		9	12	86
PVNSWCGFI	1720	2857	1174 13	9	14	100
QVVGAVLI	1721	29	1 0088	9	13	93
QVSAPSLKA	1722	2210		9	11	79
QFETLEII	1723	2808	15 0062	9	11	79
QVGFVWFLY	1724	78	15 0040	9	12	86
QFRFRFPI	1725	57	15 0039	9	13	93
RLAPITAY	1726	1029	1 0116	9	12	86
RMLMTHFF	1727	2875		9	12	86
RVCETKALY	1728	2621	1 0145	9	14	100
RMSSTKVV	1729	2252	1 0138	9	12	86
RMEIDNNY	1730	156	1 0096	9	12	86
SMITDPSEI	1731	2178	1174 10	9	14	100
SPGALVVGV	1732	1893	15 0054	9	13	93
SPGELFRVA	1733	2931	16 0015	9	11	79
SPQJRMFI	1734	2649	15 0060	9	11	79
SPGGSFSSW	1735	99	15 0042	9	11	79
SVIXNTIV	1736	1455	1 0124	9	12	86
TMKNKNEI	1737	2590		9	11	79
TIKGPIML	1738	1622	1 0129	9	11	79
TIPLSTGL	1739	686	1 0108	9	11	79
TIIGGFAH	1740	125	1 0092	9	12	86
TIWARMIM	1741	2871		9	11	79
TIPLYRGA	1742	1627	16 0017	9	13	93

Sequence	SeqID Name	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
VIETGALIA	1743	1336		9	14	100
VIETLTCGF	1744	122		9	12	86
VIETKATYA	1745	157		9	12	86
VIETIACV	1746	1852		9	11	79
VIETGALIA	1747	1666	24 0075	9	12	86
VIETPSVA	1748	1256	24 0072	9	14	100
VQWNNRRIA	1749	1918		9	14	100
VQVVCAL	1750	1898		9	11	79
VVTSIWWIV	1751	1660	1 0823	9	12	86
WNNRIIAA	1752	1920	24 0073	9	14	100
WNLVKGIA	1753	1665	40 0075	9	12	86
YPLVGAFL	1754	136	1 0817	9	11	79
YLVAYQALV	1755	1590	1 0127	9	12	86
YVTRHACV	1756	1136	1 0119	9	12	86
YQALVCAHA	1757	1594		9	13	93
YVEXCTSV	1758	276	1 0100	9	12	86
YVGVAFH	1759	637	1 0107	9	13	93
YVPESDAAA	1760	1939		9	12	86
ALVSGALVV	1761	1890	24 0101	10	12	86
ALVGVVCAA	1762	1896		10	11	79
APFPSWIXJMW	1763	1604	15 0233	10	11	79
APILWAMIL	1764	2869	15 0247	10	11	79
AGFGATWFTY	1765	77		10	12	86
AVAYFGALV	1766	1419	1 0486	10	14	100
AVCTRGVAKA	1767	1188		10	11	79
AVQWNNRRIA	1768	1917		10	14	100
GLHLLVFFL	1769	2941	1 0510	10	12	86
LVQIVVHSL	1770	1462	1 0457	10	12	86
DILAGYGAV	1771	1855	1 0495	10	11	79
DEVTSTWV	1772	1657	1 0490	10	12	86
DGVRVCEKM	1773	2617		10	13	93
DLSDGSWSIV	1774	2412	1 0499	10	11	79
DVNIIFAIL	1775	1883	1 0891	10	11	79
DQAEIAGAPL	1776	1339		10	12	86
DWKEPKKKA	1777	21	1174 01	10	12	86
ELISGSSNV	1778	2814	1 0506	10	14	100
EQEPKKAFL	1779	1731		10	12	86
EVVTSIWWIV	1780	1659	1 0491	10	12	86
GLSAFSLSHY	1781	2921	1 0509	10	11	79
GLSTIYGNFA	1782	1782		10	14	100
GLTHQALFL	1783	1569	1 0488	10	13	93
GPGRGAVQNM	1784	1912	15 0240	10	12	86
GVVGVVYLL	1785	28		10	13	93
GVQTVYHGA	1786	1081		10	11	79
GVRVCEKMAI	1787	2619	1 0504	10	14	100

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
HRQVWQYH	1788	604		10	11	79
ILAGYAGAVA	1789	1856	40 0140	10	11	79
ILGAWWAGJL	1790	1816	1 0493	10	12	86
IMAKQJVFIV	1791	2591	1 0500	10	11	79
IQYLALSLH	1792	1777		10	14	100
IVFPIIGVHV	1793	2613	1 0503	10	11	79
KPIIHGPIHL	1794	1620	15 0234	10	11	79
KVHSHLIGF	1795	121		10	12	86
KVLVIRPSVA	1796	1255		10	14	100
LLENLGGWV	1797	1812	1 0890	10	12	86
LIPAILSPGLA	1798	1887	24 0102	10	13	93
LMGVHVLVA	1799	133		10	11	79
LPAILSPGAL	1800	1888	15 0238	10	13	93
LPGFSESHF	1801	169	15 0220	10	13	93
LPKRGPRGLV	1802	37	15 0218	10	13	93
LWQDRLFF	1803	1553	15 0232	10	12	86
LWAYQATVLA	1804	1591	40 0133	10	12	86
LVDLAGYCA	1805	1853	40 0139	10	11	79
LVGAVLAALA	1806	1667		10	12	86
LVGAVVCAAI	1807	1897	40 0141	10	11	79
MLTPSHITA	1808	2179		10	14	100
NLPQSESHF	1809	168		10	13	93
NPSVAATLGF	1810	1260	15 0230	10	14	100
PIHSTLQKFL	1811	1295		10	11	79
PLGGAAHALA	1812	143		10	11	79
POFLYDLELL	1813	2807		10	11	79
PVCCXRLFEW	1814	1554	1174 14	10	12	86
PVNSWLGNIL	1815	2857		10	14	100
PVYCFIPSPV	1816	508	1 0471	10	13	93
QIPCEPEPDV	1817	2164	1 0497	10	12	86
QFEKGGIRYA	1818	2601	16 0188	10	11	79
RLHGLSAFSL	1819	2918	1 0508	10	11	79
RLVFPOLGV	1820	2611	1 0502	10	11	79
RMWDMNNRW	1821	317		10	12	86
RVLFDGWNVA	1822	156		10	12	86
SLHSYSQCEI	1823	2926	1174 15	10	11	79
SLTGRKRAV	1824	1051	1 0478	10	12	86
SPGALVVGWV	1825	1893	15 0239	10	11	79
SQISAPSLKA	1826	2209		10	11	79
SQYKGRGRJH	1827	56		10	13	93
SVAAHGFGLA	1828	1262		10	14	100
TLKGPTEPLY	1829	1622	1 0489	10	11	79
TLFNILGGW	1830	1811		10	12	86
TLFALSLGLI	1831	686	1174 03	10	11	79
TLTCGFALIM	1832	125		10	12	86

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
TPKTCGSSAL	1833	1126	15 0228	10	11	79
TPPIYHCAV	1834	1627	15 0235	10	13	93
TVNPSWIGFI	1835	2856	15 0246	10	12	86
TVHSLIPII	1836	1466		10	12	86
VDIITIGFA	1837	132		10	12	86
VLAALAAVCI	1838	1671	1 0889	10	12	86
VLDJAEIAGFA	1839	1337		10	12	86
VINPSVAAII	1840	1258	1 0483	10	14	100
VITISGRII	1841	2737	1 0505	10	11	79
VIVGVIAAI	1842	1666	1 0492	10	12	86
VVINPSVAA	1843	1256		10	14	100
VMISSYIGY	1844	2639		10	11	79
VPISDAAHIV	1845	1940	15 0241	10	12	86
VQMMNRIAF	1846	1918		10	14	100
VGVVVCAAII	1847	1898		10	11	79
WVLVGWIAA	1848	1665	40 0135	10	12	86
YIKGSSGFI	1849	1165	1 0479	10	12	86
YILPRGPIR	1850	35	1 0469	10	13	93
YIVTRHIV	1851	1136		10	11	79
YVGIIGGVF	1852	276		10	12	86
ALVVGWCAAI	1853	1896		11	11	79
APGISGSEPIV	1854	1235	29 0117	11	13	93
APTILWARMIM	1855	2869	29 0118	11	11	79
ADAPPSWIDIM	1856	1602		11	12	86
AVCTRGVAKAV	1857	1188		11	11	79
AVQMMNRIAF	1858	1917		11	14	100
DLAGYGAGVA	1859	1855		11	11	79
DLEVVTSTWVI	1860	1657		11	12	86
DLGVRCERMA	1861	2617		11	13	93
DLMGYIPIVGA	1862	132		11	11	79
DLYLVTRHIV	1863	1134		11	12	86
DGAETAGAHIV	1864	1339		11	12	86
DWKEFGGKQV	1865	21		11	12	86
EDPRKAGIL	1866	1731		11	12	86
FISGQYLAI	1867	1773		11	14	100
FLAGGSSGFA	1868	1304		11	11	79
FGGKGVVFAV	1869	24	29 0119	11	14	100
FGYSGQRMFF	1870	2646		11	11	79
GIQYLAGISII	1871	1776		11	14	100
GLPVQDRIIF	1872	1552		11	12	86
GLSLIPGRIAI	1873	1782		11	11	79
GPIPLLYRUGA	1874	1625	29 0120	11	13	93
GVAVCFIHSPIV	1875	507	29 0121	11	13	93
GVLAAALAVCI	1876	1670		11	12	86
GVRCERKMAIY	1877	2619		11	14	100

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
LVKQVLELDVDF	1878	154		11	12	86
LVKQVMDVDF	1879	696		11	11	79
LVKQVDFKDF	1880	1769		11	13	93
LVKQVDFVDF	1881	698		11	11	79
LVKDFECVDF	1882	1910		11	11	79
LVKQVVAALFA	1883	1816		11	12	86
LVKGVVDFJA	1884	1331		11	12	86
LVKGVVDFVDF	1885	1891		11	13	93
LVKGVVDFVDF	1886	2608	29 0122	11	11	79
LVKGVVDFVDF	1887	1620	29 0123	11	11	79
LVKGVVDFVDF	1888	1734		11	12	86
LVKGVVDFVDF	1889	121		11	12	86
LVKGVVDFVDF	1890	1255		11	14	100
LVKGVVDFVDF	1891	1924		11	14	100
LVKGVVDFVDF	1892	2815		11	14	100
LVKGVVDFVDF	1893	2612		11	11	79
LVKGVVDFVDF	1894	726		11	13	93
LVKGVVDFVDF	1895	1812		11	12	86
LVKGVVDFVDF	1896	1887		11	13	93
LVKGVVDFVDF	1897	36		11	13	93
LVKGVVDFVDF	1898	97		11	11	79
LVKGVVDFVDF	1899	2240		11	12	86
LVKGVVDFVDF	1900	1888	29 0124	11	12	86
LVKGVVDFVDF	1901	687	29 0125	11	12	86
LVKGVVDFVDF	1902	169	29 0126	11	13	93
LVKGVVDFVDF	1903	1553	29 0127	11	12	86
LVKGVVDFVDF	1904	1667		11	12	86
LVKGVVDFVDF	1905	1257		11	14	100
LVKGVVDFVDF	1906	1137		11	11	79
LVKGVVDFVDF	1907	1897		11	11	79
LVKGVVDFVDF	1908	1815		11	12	86
LVKGVVDFVDF	1909	2249		11	12	86
LVKGVVDFVDF	1910	1886		11	13	93
LVKGVVDFVDF	1911	168		11	13	93
LVKGVVDFVDF	1912	1295		11	11	79
LVKGVVDFVDF	1913	2403		11	13	93
LVKGVVDFVDF	1914	2667		11	11	79
LVKGVVDFVDF	1915	1606	29 0128	11	11	79
LVKGVVDFVDF	1916	2857		11	12	86
LVKGVVDFVDF	1917	508		11	13	93
LVKGVVDFVDF	1918	635		11	13	93
LVKGVVDFVDF	1919	2243		11	12	86
LVKGVVDFVDF	1920	2621		11	13	93
LVKGVVDFVDF	1921	175		11	12	86
LVKGVVDFVDF	1922	2178		11	14	100

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
SPDHYVPE SDA	1923	1935	29 0129	11	12	86
SAHYEPEPEV	1924	2163		11	12	86
SVAAHUGGAY	1926	1262		11	14	100
ELGCGAMSKA	1926	1266	29 0130	11	12	86
HEENEGWW	1927	1831		11	12	86
PECTGSSRY	1928	1126		11	11	79
HYAFVCEH	1929	1550	29 0131	11	13	93
TPVNSWIGRI	1930	2856	29 0132	11	12	86
IVLDQAF TAGA	1931	1336		11	12	86
VLGCHWGA	1932	1521		11	11	79
VLVHLAGYGA	1933	1852	29 0133	11	11	79
VLVGVLAAL A	1934	1666		11	12	86
VGFKGGRPA	1935	2600		11	11	79
VGVNRIHIA	1936	1918	29 0134	11	14	100
VVCALHFRIV	1937	1901		11	11	79
WVLVGVLAAL	1938	1665		11	12	86
VIKSSGgRI	1939	1165	29 0135	11	12	86
VIVATGATVCA	1940	1590		11	12	86
YCATVCAAGJA	1941	1594		11	11	79
YVHRCGSRI	1942	276	29 0136	11	12	86
YVHSQAAHIV	1943	1939		11	12	86

Table XV
HCV A01 Motif with Binding Information

Sequence	SeqID Num	Position	Pepptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101
ASGCGSPY	1944	166	26 0026	8	20	100	0 0001
DREVLSPKY	1945	737	20 0255	10	18	90	0 0680
FAAFEGCGY	1946	631	20 0254	10	19	95	
GAATLCKGY	1947	630		11	19	95	
GRETVLEY	1948	140		8	15	75	
GYSLEMGY	1949	579	2 0058	9	17	85	
HLLWKAGLY	1950	149	1069 04	10	20	100	0 1100
KQAFTEPTLY	1951	653	20 0256	10	19	95	0 0001
LLDIALALY	1952	30	1069 01	9	17	85	1 2 0000
LSLVSAALY	1953	415	1090 07	10	19	95	0 0150
LTGRETVLEY	1954	137		11	15	75	
MMWVWGPSLY	1955	360	1039 01	10	17	85	0 0810
MSITTELY	1956	103	2 0126	9	15	75	0 8500
NSVLSRPY	1957	738	2 0123	9	18	90	0 0005
PLDKGKPY	1958	124	1147 12	9	20	100	
PLDKGKPY	1959	124	1069 03	10	20	100	0 1700
PLIGRTSLY	1960	797	1090 09	9	17	85	0 2100
SASICGSPY	1961	165		9	20	100	
SLDVSAALY	1962	416	1069 02	9	19	95	5 2000
STIDLEAY	1963	104		8	15	75	
TTGRTSLY	1964	798	26 0030	8	17	85	
WLSLVSAALY	1965	414	26 0551	11	19	95	
WMMWVWGPS	1966	359	1039 06	11	17	85	0 3200
YFAIMFLY	1967	640	19 0014	8	19	95	
YSLNFMGY	1968	580	26 0032	8	17	85	

Table XVI

HCV A03 Morph with Binding Information

Concavity	Freq	Peptide	Start	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
86	12	24 0103	.	647	10	AACNTRGER	1969	0.0003
79	11			147	10	AARALAHGVR	1970	
100	14			1264	8	AATLGFGA	1971	
100	14			1264	9	AATLGFGAY	1972	
79	11	24 0104 40 0089	.	1187	9	AAVCTRGVA	1973	0.0003
79	11			1187	10	AAVCTRGVAK	1974	
79	11			1187	11	AAVCTRGVAKA	1975	
86	12			648	9	ACNTRGER	1976	
79	11			1306	9	AUGGUSGGA	1977	
79	11			1306	10	AUGGUSGAY	1978	
86	12			1142	8	ADVIPRR	1979	
79	11			1142	9	ADVIPRRR	1980	
100	14			1926	8	AFASRGNH	1981	
86	12			1865	8	AGALVAFK	1982	
86	12	24 0104 40 0089	.	1344	9	AGARLVLA	1983	0.0003
79	11			1344	11	AGAFVLATA	1984	
100	14			1781	11	AGLSTLPNPA	1985	
86	12			1862	9	AGVAGALVA	1986	
86	12			1862	10	AGVAGALVAF	1987	
86	12			1862	11	AGVAGALVAFK	1988	
86	12			94	8	AGWLLSPR	1989	
86	12			94	11	AGWLLSPHSR	1990	
86	12			1858	8	AG ^W GAGVA	1991	
86	12			1858	10	AG ^W GAGVAGA	1992	
86	12	24 0104 40 0089	.	1737	8	ALGLOTA	1993	0.0003
86	12			689	8	ALSTGLH	1994	
86	12			689	10	ALSTGLHLH	1995	
79	11			1896	9	ALVWGWCA	1996	
79	11			1896	10	ALVGVVCAA	1997	
79	11			1793	8	ASLMAFTA	1998	
79	11			2208	10	ASQLSAPSLK	1999	
79	11			2208	11	ASQLSAPSLKA	2000	
86	12			1928	11	ASRCNHSPTH	2001	
100	14			2204	10	ASSASQLSA	2002	
93	13	1090 23	.	165	10	ATGNLPGCSF	2003	0.0260
100	14			1265	8	ATLFGAY	2004	
86	12			1265	11	ATL ^G GAYMSK	2005	
79	11			48	8	ATHKTSR	2006	
79	11			1596	9	ATVCARAQA	2007	
79	11			1188	8	AVCTRGVA	2008	
79	11			1188	9	AVCTRGVAK	2009	
79	11			1188	10	AVCTRGVAKA	2010	
100	14			1917	10	AVQVMNRLIA	2011	
100	14			1917	11	AVQVMNRLIAF	2012	
93	13			1903	8	CAAILRRH	2013	

Consistency	Freq	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
79	11			1530	9	CAWVELTPA	2014	
93	13			128	9	CGFADLMGY	2015	
79	11			2742	8	CNTILTCY	2016	
79	11			1130	11	CGSSDLYLVR	2017	
100	14			2727	8	CGYRRCRA	2018	
86	12			2941	11	CLPKLVPPLR	2019	
100	14			172	9	CSFSIFLA	2020	
100	14			2819	8	CSSNVSA	2021	
86	12			2819	9	CSSNVSAH	2022	
79	11			1128	9	CLGSSULY	2023	0.0001
79	11			1190	8	CIRGVAKA	2024	
79	11			1190	11	CIEGVAKAVDF	2025	
79	11			555	9	CTWMNSTGF	2026	
79	11			555	11	CTWMNSTGFTK	2027	0.7600
79	11			2599	9	CVDFEKGR	2028	0.0008
79	11			2599	10	CVDFEKGRK	2029	0.0011
86	12			1462	8	CVTQVDF	2030	
100	14			1574	9	DAIFLSQTK	2031	0.0003
79	11			2771	10	DELWICESA	2032	
100	14			1468	8	DFSLDPTF	2033	
79	11			1307	8	DGGGSGGA	2034	
79	11			1307	9	DGKSGGAY	2035	
86	12			1316	9	LIHICDECH	2036	
86	12			1855	8	DILAGYGA	2037	
79	11			1855	11	DILAGYGAGA	2038	
93	13			2617	9	DIGRVCEK	2039	0.0003
93	13			2617	11	DLGVRVCEKMA	2040	
79	11			132	11	DLMGYPLVGA	2041	
79	11			1883	8	DLVNLPA	2042	
79	11			2772	9	DLWICESA	2043	
79	11			1134	8	CLYLVTRH	2044	
86	12			1134	9	DLYLVTRHA	2045	0.0003
86	12			124	8	DLTTCGFA	2046	
79	11			1143	8	DVIPVRRR	2047	
100	14			2794	8	EAMTRYSA	2048	
79	11			1524	8	E_YUAGJA	2049	
79	11			1524	10	ECYDAGCAWY	2050	
79	11			1882	9	EDLVNLLPA	2051	
100	14			1915	9	EGAVQWMINR	2052	0.0004
93	13			1377	8	EIPFYGA	2053	
86	12			2245	8	EMGNTR	2054	
86	12			1342	11	ETAGARLVLA	2055	
86	12			1207	9	ETIMRSPVF	2056	
86	12			2596	9	EVFQVDEK	2057	0.0008
79	11			2598	10	FCVDFEKGR	2058	

Conservation	Freq	Exptl	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
79	11			2598	11	FCVCFKGGH	2059	
86	12			1269	8	FGAYNSKA	2060	
86	12			1263	9	FGAYNSKAH	2061	
79	11			553	11	FGCTWNNSTGF	2062	
86	12	3.0060		2554	9	FGTGAKDVR	2063	0.0008
100	14	40.0082		1773	9	FSGIOYLA	2064	
79	11			1304	11	FLAKYKSGDA	2065	
100	14			728	8	FLLADAR	2066	
79	11			2670	8	FSYDTRCF	2067	
100	14			2792	8	FTEAMTRY	2068	
100	14			2792	10	FTEAMTRYSA	2069	
93	13			1567	9	FTGLTHIDA	2070	
93	13			1567	10	FTGLTHIDAH	2071	
93	13			1567	11	FTGLTHIDAHF	2072	
79	11			146	8	GAARALAH	2073	
79	11			146	11	GAARALAHGVR	2074	
86	12			1861	10	GAGVAGALVA	2075	
86	12			1861	11	GAGVAGALVAF	2076	
86	12			350	8	GAHWGVLA	2077	
79	11			1895	10	GALVVGWCA	2078	
79	11			1895	11	GALVVGWCAA	2079	
79	11			1345	8	GARLVLA	2080	
79	11			1345	10	GARLVLATA	2081	
100	14			1916	8	GAVQWNNR	2082	
100	14			1916	11	GAVQWNNRLIA	2083	
86	12			1270	8	GAYMSKAH	2084	
79	11			1529	10	GCAWYELTPA	2085	
100	14			171	10	GCFSIFLLA	2086	
79	11			554	10	GCTWNNSTGF	2087	
79	11			2770	11	GDOLVICESA	2088	
86	12			278	8	GDLCGVF	2089	
93	13			129	8	GFADLMGY	2090	
86	12			1268	8	GFGAYMSK	2091	
86	12			1268	9	GFGAYMSKAH	2092	
86	12			1268	10	GFGAYMSKAH	2093	
79	11			2645	9	GFGNSPGR	2094	
79	11			2663	9	GFSYDTRCF	2095	
79	11			145	8	GGAARALA	2096	
79	11			145	9	GGAARALAH	2097	
79	11			1308	8	GGLSGGAY	2098	
100	14			26	10	GGLSGGAY	2099	
79	11			935	8	GGLSGGAY	2100	
100	14			27	9	GGLSGGAY	2101	
100	14	24.0078		1392	9	GGRHUFCH	2102	0.0003
100	14			1392	11	GGRHUFCHSK	2103	

Conservation	Freq	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
79	11			2695	11	GGKPAHVF	2104	
86	12			1669	8	GGVLAAL	2105	
86	12			1669	9	GGVLAALAA	2106	
86	12			1669	10	GGVLAALAA	2107	
93	13			32	8	GGVLLPR	2108	
93	13	24-0380		32	9	GGVLLPRR	2109	0.0003
86	12			1818	9	GGWAAOLA	2110	
100	14			1333	9	GIGVLDOA	2111	
79	11			3037	8	GIVLLPR	2112	
93	13			1552	8	GLPVODH	2113	
86	12			1552	11	GLPVODHLEF	2114	
79	11			1004	8	GLPVSARR	2115	
79	11			968	8	GLDLAVA	2116	
79	11			2921	8	GLSAFSLH	2117	
79	11	1073-03		2921	10	GLSAFSLHSY	2118	0.0100
100	14			1782	10	GLSTLPNPA	2119	
93	13			1569	8	GLTHDAH	2120	
93	13			1569	9	GLTHDAHF	2121	
86	12			1238	10	GSGKSTKPA	2122	
86	12			1238	11	GSGKSTKPAA	2123	
86	12			1131	10	GSSDLYLVR	2124	
86	12			1131	11	GSSDLYLVTRH	2125	
79	11			2641	8	GSSYGFY	2126	
79	11			2063	8	GTFPINAY	2127	
100	14			1335	10	GTVLDOAETA	2128	
86	12			1863	8	GVAGALVA	2129	
86	12			1863	9	GVAGALVAF	2130	
79	11	1073-10		1863	10	GVAGALVAFK	2131	0.3900
79	11			1193	8	GVAKAVDF	2132	
79	11			1081	8	GVQWTVYH	2133	
79	11			1081	10	GVQWTVYHGA	2134	0.0014
79	11	1090-25		3035	10	GVGYLPR	2135	
86	12			1670	8	GVLAALAA	2136	0.0046
86	12	1174-19		1670	9	GVLAALAA	2137	
79	11			45	11	GVRAIRKTSER	2138	
100	14			2619	9	GVRCERMA	2139	
100	14			2619	11	GVRCERMA	2140	
86	12			154	11	GVRLDGNY	2141	
79	11			1900	9	GVCAAILR	2142	
79	11			1900	10	GVCAAILRR	2143	
79	11			1900	11	GVCAAILRRH	2144	
93	13			33	8	GVLLPR	2145	
93	13			33	11	GVLLPRGFR	2146	
79	11			1141	8	HADVIPR	2147	
79	11			1141	9	HADVIPRR	2148	

Conservancy	Freq	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
79	11			1141	10	HADVIPRRR	2149	
100	14			1234	8	HAPTGSQK	2150	
93	13			1234	11	HAPTGSQSKTK	2151	
79	11			2920	9	HGLSAFSLH	2152	
79	11			2920	11	HGLSAFSLHSY	2153	
79	11			1624	8	HGPTPLLY	2154	
79	11			1624	9	HGPTPLLYR	2155	
100	14			1572	11	HIDAFLSQTK	2156	0.5900
86	12			1232	10	HLHWFGSK	2157	
79	11			696	11	HLHONIVDQY	2158	
100	14			1395	8	HLFCHSK	2159	
100	14			1395	9	HLFCHSKA	2160	0.0250
100	14			1395	10	HLFCHSKK	2161	0.0260
93	13			1769	11	HMNHISGIUY	2162	
100	14			1400	10	HSKKKIDELA	2163	
100	14			1400	11	HSKKKIDELAA	2164	
79	11			2928	10	HSYSGEINR	2165	
79	11			222	10	HIPGCVPCVR	2166	0.0004
79	11			1910	8	HVQREGA	2167	
79	11			1925	9	IAFASRGNIH	2168	0.0003
100	14			1573	10	IDAHFLSQTK	2169	
100	14			123	8	IDTLTQGF	2170	
86	12			123	9	IDTLTGFA	2171	
86	12			1397	8	IFCHSKK	2172	
100	14			1334	8	IGTVLDQA	2173	
100	14			1334	11	IGTVLDQAETA	2174	
86	12			1317	8	IICDECH	2175	
79	11			1856	10	ILAGYGAGVA	2176	
86	12			1816	8	ILGGWVAA	2177	
86	12			1816	11	ILGGWVAAQLA	2178	
86	12			1331	11	ILGIGTVLDQA	2179	
86	12			2591	8	IMAKNEF	2180	
100	14			1774	8	ISGIOYLA	2181	0.0150
86	12			2250	9	ITRVESENF	2182	
100	14			2816	11	ITSCSSNVSVIA	2183	
86	12			989	8	ITWGADTA	2184	
86	12			989	9	ITWGADTAA	2185	
86	12			1296	8	ITYSTYQK	2186	
86	12			1296	9	ITYSTYQKF	2187	
79	11			1296	11	ITYSTYQKTLA	2188	
86	12			701	8	IVDVJLY	2189	0.0036
79	11			2613	9	IVFDLQVR	2190	0.0008
93	13			30	10	IVGGVILLPR	2191	
93	13			30	11	IVGGVILLPRR	2192	
86	12			1736	9	KALGLGLTA	2193	

Concurrence	Freq	Peptide	Filled	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
86	12			1404	8	KCEIAAK	2194	
86	12			2553	10	KFGYGAQVR	2196	
79	11			1391	8	KGGRIHF	2196	
79	11			1391	10	KGGRIHFCH	2197	
79	11			2604	8	KGGRIKPAR	2198	
86	12			2944	8	KLGVPPIR	2199	
86	12			1241	8	KSTKVPAA	2200	
86	12	13 0016		1241	9	KSTKVPAAI	2201	0 0009
86	12			1241	10	KSTKVPAAIA	2202	
79	11			1241	11	KSTKVPAAIYA	2203	
86	12			10	8	KTKRNTNR	2204	
86	12			10	9	KTKRNTNR	2205	0 0110
93	13	24 0085		51	9	KTSRSQPR	2206	0 1600
86	12	1 0952		51	11	KISEHSJHGR	2207	
86	12			121	10	KVIDLTGGF	2208	
86	12			121	11	KVIDLTGGA	2209	
100	14			1255	10	KVALVNPSVA	2210	
100	14			1255	11	KVLVNPSVAA	2211	
79	11			1244	8	KVPAAYAA	2212	
79	11			1305	10	LADGASGGA	2213	
79	11			1305	11	LADGASGGAY	2214	
86	12			1729	8	LAQIFPK	2215	
86	12			1729	9	LAQIFPKA	2216	
79	11			1857	9	LAGEFKKA	2217	
79	11			1857	11	LAGEFKKGA	2218	
79	11			1522	10	LELYLAGLA	2219	
86	12			1338	9	LDOAETAG	2220	
86	12			1338	10	LDOAETAGAR	2221	
100	14			727	8	LFLLADA	2222	
100	14			727	9	LFLLADAR	2223	
86	12			1813	10	LFNILGGWA	2224	
86	12			1813	11	LFNILGGWNA	2225	
79	11			290	8	LFTEPRR	2226	
86	12	24 0086		1267	9	LGFAYMSA	2227	0 0810
86	12			1267	10	LGFAYMSKA	2228	
86	12			1267	11	LGFAYMSKAH	2229	
79	11			144	9	LGAHAHALA	2230	
79	11			144	10	LGAHAHALAH	2231	
86	12			1817	10	LGGWAAGLA	2232	
93	13			1332	10	LGGTLDGA	2233	
86	12			44	8	LGVRAIRK	2234	
100	14			2619	8	LGVRAIRK	2235	
100	14			2618	10	LGVROCKMA	2236	
100	14			1924	10	LIAFASGRNH	2237	
86	12	1 0959		2235	9	LEANLWR	2238	0 0008

Conservancy	Freq	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0.001
100	14			1396	8	LIFCHSKK	2239	
100	14	1 01273	.	1396	9	LIFCHSKK	2240	0.5406
79	11			414	9	LNITNGSWH	2241	
79	11	1 1066		2612	10	LVFPDLGVR	2242	0.0003
100	14			1030	8	LLAPITAY	2243	
100	14			726	9	LLFTLLADA	2244	0.0016
100	14	24 0071	.	726	10	LLFTLLADAR	2245	
100	14	1090 28	.	726	11	LLFNILGWA	2246	
86	12			1812	10	LLPAILSPGA	2247	0.0003
93	13	24 0102		1887	8	LLPRRGPR	2248	
93	13			36	8	LLSPRGSR	2249	
86	12			97	8	LLSPRGSR	2250	
79	11			133	10	LMGYPLVGA	2251	0.0002
79	11	13 0019	.	2922	9	LSATSLHSY	2252	
79	11			2211	8	LSAPSLKA	2253	
86	12			2479	8	LSISLRLH	2254	0.0003
86	12	24 0087		2479	9	LSISLRLH	2255	
86	12			690	9	LSTGLHLH	2256	
100	14			1783	9	LSTGLHFA	2257	
86	12			126	11	LTCGFADLMGY	2258	
100	14			2180	9	LTDPSHTA	2259	
93	13			1570	8	LTHDAHF	2260	
93	13			2176	10	LTSMLTDFSH	2261	
86	12	40 0133		1591	10	LVAYGATVCA	2262	
79	11			1591	11	LVAYQATVCAR	2263	
79	11			1853	8	LVDILAGY	2264	
79	11	40 0139		1853	10	LVDILAGYGA	2265	
86	12			1667	8	LVGGVLAA	2266	
86	12			1667	10	LVGGVLAALA	2267	
86	12			1667	11	LVGGVLAALAA	2268	
100	14			1257	8	LVLNFSVA	2269	
100	14			1257	9	LVLNFSVA	2270	
79	11			1897	8	LVGGVCAA	2271	
79	11			1897	9	LVGGVCAA	2272	
79	11			2773	8	LWICESA	2273	
79	11			2668	8	MGFSYDIR	2274	
79	11			2668	10	MGFSYDHF	2275	
79	11			2640	9	MGFSYDFY	2276	
79	11			134	9	MGYPLVGA	2277	
79	11			2876	8	MILMTHFF	2278	
86	12			2179	10	MLTDFSHITA	2279	
100	14			1	9	MSTNPKPQR	2280	
79	11			1	10	MSTNPKPQHP	2281	
79	11			2726	8	NCGYRRCR	2282	
79	11			2726	9	NCGYRRCRA	2283	
79	11			305	8	NCSYPPGH	2284	

Concordance	Frq	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0303
100	14			1772	8	NFISGIQY	2284	
100	14			1772	10	NFISGIQYLA	2285	
79	11			1080	8	NGVCWTVY	2286	
79	11			1080	9	NGVCWTVYH	2287	
79	11			1080	11	NGVCWTVYHGA	2288	
86	12			1815	8	NILGGWA	2289	
86	12			1815	9	NILGGWAA	2290	
86	12	1 0438		2249	10	NITRVESENK	2291	0 0010
86	12	1073 01		700	9	NIMDVQYLY	2292	0 0005
93	13			1886	11	NLLPAILSPGA	2293	
93	13			168	10	NLPQCSFIF	2294	
86	12			1460	10	NITCVTQTVDF	2295	
79	11			14	10	NINRRPDVK	2296	
79	11	2 0168		14	11	NINRRPDVKF	2297	0 0010
93	13			1549	11	NIPGLFVCOOH	2298	
93	13			1889	8	PAILSPGA	2299	
86	12			688	9	PALSTGLIH	2300	
86	12			688	11	PALSTGLIHL	2301	
79	11			1976	8	PCSGSWLR	2302	
79	11			1127	10	PCITGSSQLY	2303	
93	13			2616	10	PDLGVVCEK	2304	
79	11			1894	11	PGALVVGWCA	2305	
100	14			170	8	PGCSFIF	2306	
100	14			170	11	PGCSFIFLLA	2307	
86	12			224	8	PGCVPLVF	2308	
93	13			1913	11	PGEGAVMMNR	2309	
79	11			2932	8	PGEINRVA	2310	
86	12			1509	9	PGERPSGMF	2311	
100	14			25	11	PGGGWGGVY	2312	
93	13			1551	9	PGLPWGJOH	2313	
100	14			79	8	PGYWPPLY	2314	
79	11			1295	9	PIITYSTYCK	2315	
79	11			1295	10	PIITYSTYCKF	2316	
79	11			143	8	PLGGAARA	2317	
79	11			143	10	PLGGAARALA	2318	
79	11			143	11	PLGGAARALAH	2319	
93	13			1628	8	PLLYRLGA	2320	
79	11			2667	9	PMGFSDYIR	2321	
79	11			2667	11	PMGFSDYIRCF	2322	
93	13			514	11	PSPVVVGTTDR	2323	
100	14			1261	9	PSVAATLGF	2324	
100	14			1261	11	PSVAATLGFSA	2325	
79	11			1607	8	PSWDDMMK	2326	
93	13			587	8	PIDCFRKH	2327	
86	12	1 0954		109	9	PIDCFRRSR	2328	0 0008

Conservation	Length	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
93	13	1 0121		1236	9	PTSSGKSLK	2329	0 0002
86	12			1936	10	PTHVPESDA	2330	
86	12			1936	11	PTHVPESDA	2331	
79	11			1621	11	PTLHGPTLLY	2332	
93	13			1626	10	PTLLYRLGA	2333	
86	12			1554	9	PVOOHLEF	2334	
93	13	1 0956		516	9	PWWGIIIDR	2335	0 0008
86	12			1340	8	QAEIAGAR	2336	
93	13			1595	8	QATVGARA	2337	
79	11			1595	10	QATVCARQJA	2338	
93	13			29	11	QINGGVLLPR	2339	
86	12			289	8	QLTFSPR	2340	
79	11	1 0955		289	9	QLTFSPRR	2341	0 7500
86	12			336	8	QLLRIPQA	2342	
79	11			2219	8	QLSAPSLK	2343	
79	11			2210	9	QLSAPSLKA	2344	
86	12			1465	11	QVDFSLDPTF	2345	
79	11			1186	10	RAAVCTRGVA	2346	
79	11			1186	11	RAAVCTRGVAK	2347	
100	14			149	8	RALAHGVR	2348	
79	11			47	9	RATKTSEK	2349	
86	12	24 0088		1930	9	RGNHNSPTH	2350	0 0003
86	12	24 0105		1930	10	RGNHNSPTHY	2351	0 0003
93	13			40	8	RGPRLGVR	2352	
93	13			40	9	RGPRLGVRA	2353	
79	11			40	11	RGPRLGVRATR	2354	0 0120
93	13	24 5081		59	9	RGRHJPIK	2355	
86	12			1154	8	RGSLLSPR	2356	
79	11			1192	9	RGVAKVDF	2357	
79	11			43	8	RLGVRATR	2358	
79	11	1073 11		43	9	RLGVRATRK	2359	0 9400
86	12			2918	8	RLHGLSAF	2360	
79	11			2918	11	RLHGLSAFLH	2361	
100	14			1923	8	RLIAFASR	2362	
100	14			1923	11	RLAFASRGNH	2363	
79	11			2611	11	RLVFPDLGVR	2364	
86	12			1029	8	RLAPITA	2365	
86	12	1174 18		1029	9	RLAPITAY	2366	2 7000
86	12			1347	8	RLVVIATA	2367	
86	12			2875	8	RLMLTHF	2368	
86	12			2875	9	RLMLTHFF	2369	
100	14			635	9	RLMYGGVEH	2370	
100	14	1073 13		635	10	RLMYGGVEHR	2371	0 7200
93	13			55	8	RSQPRGR	2372	
100	14	1174 21		2621	9	RYCEKNALY	2373	0 1800

Conservancy	Freq	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
86	12	1174 17	.	156	9	RVEDGVNR	2374	0 0120
86	12			156	10	RVLEDGVNFA	2375	
79	11			2923	8	SAFSLHSY	2376	
79	11			2207	11	SASQLSAPSLK	2377	
100	14			2818	9	SCSSNVSA	2378	
86	12			2818	10	SCSSNVSAH	2379	
86	12			1133	8	SDLYLVTR	2380	
86	12			1133	9	SDLYLVTRH	2381	
86	12			1133	10	SDLYLVTRHA	2382	
100	14			173	8	SFSFLA	2383	
86	12			1239	9	SGKSTKVPFA	2384	
86	12			1239	10	SGKSTKVPFAA	2385	
86	12			1239	11	SGKSTKVPFAAY	2386	
100	14			2178	8	SMLTDPSTH	2387	
100	14			2178	11	SMLTDPSTHIA	2388	
100	14			2206	8	SSASQLSA	2389	
86	12	24 0089		1132	9	SSDLYLVTR	2390	0 0003
86	12	24 0106		1132	10	SSDLYLVTRH	2391	0 0003
86	12			1132	11	SSDLYLVTRHA	2392	
100	14			2820	8	SSNVSAH	2393	
86	12			2205	9	SSASQLSA	2394	
86	12			691	8	STGLJLH	2395	
86	12			1242	8	STKVFAAAT	2396	
86	12			1242	9	STKVFAAATA	2397	
79	11			1242	10	STKVPAATAA	2398	
100	14			1784	8	STLPGNFA	2399	
79	11			2	8	STNPKFOR	2400	
79	11			2	9	STNPKFOR	2401	
79	11			2	11	STNPKFORRTK	2402	
86	12			1663	11	STWLVGGVLA	2403	
86	12			1299	8	STYGLFLA	2404	
100	14			1262	8	SVAATLGF	2405	
100	14			1262	10	SVAATLGF GA	2406	
100	14			1262	11	SVAATLGF GAY	2407	
86	12			1343	10	TAGARLVLA	2408	
93	13			127	10	TGFAADLMG	2409	
79	11			1129	8	TGSSDLY	2410	
86	12			1461	9	TCVTQTVD	2411	
86	12			110	8	TDPRTSR	2412	
100	14			2181	8	TDPSTHA	2413	
79	11			1375	9	TGEIFFYGLK	2414	
79	11			1375	10	TGEIFFYGLKA	2415	
93	13			1568	8	TGLTHICA	2416	
93	13	24 0082		1568	9	TGLTHIDAH	2417	0 0003
93	13			1568	10	TGLTHIDAHF	2418	

Consistency	Find	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
93	13			166	9	TGNIPOCSF	2419	
93	13			1237	8	TGNAKSLK	2420	
86	12			1237	11	TGSGKTKVPA	2421	
79	11			2590	9	TIMAKNEVF	2422	
86	12	1073 14	*	1266	10	TIGHGATMSK	2423	0 0810
86	12			1266	11	TILGFATMSKA	2424	
79	11	1073 04	*	1622	10	TLHGPTLLY	2425	0 0830
79	11			1622	11	TLHGPTLLYR	2426	
79	11			686	11	TLPALSTGLIH	2427	
79	11			2871	11	TLWARMILMTH	2428	
100	14			2817	10	TSCSSNVSA	2429	
86	12			2817	11	TSCSSNVSAH	2430	
93	13			52	8	TSESRQR	2431	
86	12	24 0107		52	10	TSESRQRGR	2432	0 0003
86	12			52	11	TSESRQRGR	2433	
86	12			1050	8	TSLIGHUK	2434	
93	13	24 0083		2177	9	TSMITDPSH	2435	0 0003
79	11			2589	10	TTIMAKNEVF	2436	
86	12			1208	8	TTMRSPVF	2437	
79	11			1597	8	TVCARQA	2438	
86	12			1466	10	TVDFSLDPTF	2439	
100	14			1336	9	TVLDOAETA	2440	
86	12			1336	11	TVLDOAETAGA	2441	
100	14			1263	9	VAATLGFGA	2442	
100	14			1263	10	VAATLGFAGY	2443	
86	12			1864	8	VAGALVAF	2444	
86	12	24 0090	*	1864	9	VAGALVAFK	2445	0 2400
86	12	40 0071	*	1592	9	VAYOATVCA	2446	
79	11	1 1064	*	1592	10	VAYOATVCAR	2447	0 0005
79	11			1592	11	VAYOATVCARA	2448	
79	11			1902	8	VCAAILRR	2449	
79	11			1902	9	VCAAILRRH	2450	
100	14			2622	8	VCEKMALY	2451	
93	13			505	8	VCGPVYCF	2452	
86	12			1555	8	VCOXKLEF	2453	
79	11			1189	8	VCTRGVAK	2454	
79	11			1189	8	VCTRGVAKA	2455	
79	11			1082	9	VQWTVYHGA	2456	
100	14			1467	9	VDFSLDPTF	2457	
79	11			1854	9	VDILAGTGA	2458	
93	13			614	9	VDYPRILWH	2459	
93	13			614	10	VDYPRILWHY	2460	
86	12			2597	8	VFCVQPEK	2461	
79	11			2597	11	VFCVQPEKGR	2462	
79	11			2614	8	VFPDLGVR	2463	

Consistency	Freq	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0.30.1
93	13			1566	10	VFTGLTHIDA	2464	
93	13			1566	11	VFTGLTHIDAH	2465	
86	12			277	9	VGDLGGSVF	2466	
86	12			1668	9	VGGVLAALA	2467	
86	12			1668	10	VGGVLAALAA	2468	
86	12			1668	11	VGGVLAALAA	2469	
93	13	24.0084		31	9	VGGVLLPR	2470	0.0003
93	13			31	10	VGGVLLPRR	2471	
79	11	1.104.01		3036	9	VGVLLPNR	2472	0.0007
79	11			1899	10	VGWCAAILR	2473	
79	11			1899	11	VGWCAAILRR	2474	
86	12			122	9	VDTLTGFA	2475	
86	12			122	10	VDTLTGFA	2476	
86	12			1671	8	VLAALAA	2477	
93	13			1521	8	VLECYDA	2478	
79	11			1521	11	VLECYDA	2479	
100	14			1337	8	VLDQAEIA	2480	
86	12			1337	10	VLDQAEIAGA	2481	
86	12			1337	11	VLDQAEIAGAR	2482	
86	12			157	8	VLEDGVNY	2483	
86	12			157	9	VLEDGVNYA	2484	
100	14			1258	8	VLNPSVAA	2485	
93	13			2175	11	VLTSMLTDP SH	2486	
79	11			1852	9	VLVDILAGY	2487	
79	11			1852	11	VLVDILAGYGA	2488	
86	12			1666	8	VLVGGLA	2489	
86	12	24.0075		1666	9	VLVGGLAA	2490	0.0003
86	12			1666	11	VLVGGLAALA	2491	
100	14	24.0072		1256	9	VLVLNPSVA	2492	0.0003
100	14			1256	10	VLVLNPSVAA	2493	
79	11			2639	8	VMGSSYGF	2494	
79	11			2639	10	VMGSSYGF	2495	
79	11			1138	11	VTRHADVIPVR	2496	
79	11			1901	8	VVCAAILR	2497	
79	11			1901	9	VVCAAILRR	2498	
79	11			1901	10	VVCAAILRRH	2499	
79	11			1898	8	VWGVVCAA	2500	
79	11			1898	11	VWGVVCAAILR	2501	
93	13			517	8	VWGTIDR	2502	
86	12			93	9	WAGWLSFR	2503	
86	12			1766	8	WAKHWNF	2504	
86	12			76	11	WAGPGYWF1Y	2505	
86	12			2873	9	WARMILMTH	2506	
86	12			2873	10	WARMILMTHF	2507	
86	12			2873	11	WARMILMTHFF	2508	

Conservative	From	Peptide	File 3	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
86	12			107	8	WGPTDPRR	2509	
86	12			107	9	WGPTDPRRR	2510	
86	12			107	11	WGPTDPRRRSR	2511	
86	12	1 0953		95	9	WLLSPRCSR	2512	0 0008
100	14			1920	8	WMNRLIAF	2513	
100	14	24 0073		1920	9	WMNRLIAFA	2514	0 0003
100	14			1920	11	WMNRLIAFSR	2515	
79	11	1174 16		557	9	WMNSTGFTK	2516	0 0530
86	12	40 0075		1655	9	WWLVGGVLA	2517	
86	12	40 0135		1655	10	WWLVGGVLA	2518	
86	12			164	11	YATGNLPGLSF	2519	
79	11			1526	8	YDAGCAWY	2520	
86	12			1315	10	YDIICDECH	2521	
86	12			1850	8	YGAGVAGA	2522	
86	12			1850	11	YGAGVAGALVA	2523	
79	11			2644	10	YGFQYSPGQR	2524	
93	13	1 0951		35	9	YLLPRRGPR	2525	0 0054
86	12			1590	11	YLVAYQATVCA	2526	
79	11			2930	8	YSPGEINR	2527	
79	11			2930	10	YSPGEINRVA	2528	
79	11			2648	9	YSPQRVEFF	2529	
86	12			1298	9	YSTYGKFLA	2530	
86	12			276	10	WGDLCGSVF	2531	
100	14			637	8	YVGVEHR	2532	
86	12			1939	8	YVPESDAA	2533	
86	12			1939	9	YVPESDAAA	2534	
86	12	1 1065		1939	10	YVPESDAAAR	2535	0 0003

Table XVII

HCV All Motif with Binding Information

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101
AACNWIRGER	2536	647	24 0103	10	12	86	0 0140
AARAIARIGVR	2537	147		10	11	79	
AAITLFGAY	2538	1264		9	14	100	
AAVLTIRIVAK	2539	1187		10	11	79	
ACNWIRGER	2540	648		9	12	86	
ALXLFSGAY	2541	1306		10	11	79	
ALVIVRR	2542	1142		8	12	86	
ALVIVRRR	2543	1142		9	11	79	
ALVIRRH	2544	1926		8	14	100	
AGALVAK	2545	1865		8	12	86	
AGVAVALVAK	2546	1862		11	12	86	
AGWLTSPH	2547	94		8	12	86	
AGWLTSPKSR	2548	94		11	12	86	
ALVGLIH	2549	689		8	12	86	
ALSTLPHH	2550	689	24 0104	10	12	86	0 0027
ASQISAPSK	2551	2208		10	11	79	
ASRGPRVSPH	2552	1928		11	12	86	
ATLIGAY	2553	1265		8	14	100	
ATLIGAYMSK	2554	1265		11	12	86	
ATHKTSR	2555	48		8	11	79	
AVLTIRIVAK	2556	1188	1090 23	9	11	79	0 0250
CAAEIRH	2557	1903		8	13	93	
CGFALIMGY	2558	128		9	13	93	
GLNLTLY	2559	2742		8	11	79	
GLSSRLVTH	2560	1130		11	11	79	
GLRKLGVPLR	2561	2041		11	12	86	
GNLSIPGH	2562	304		9	11	79	
GNWIRER	2563	649		8	12	86	
GSSNVSVAH	2564	2819		9	12	86	
GLGLSSALY	2565	1128	1069 62	9	11	79	0 0063
GLWNLSIGLIR	2566	555	3 0438	11	11	79	0 7500
GVLFKLF	2567	2599	1 0961	9	11	79	0 0005
GVLFKLFPR	2568	2599	1 0501	10	11	79	0 0008
DAFLSQTR	2569	1574	24 0076	9	14	100	0 0005
DLXFSQAY	2570	1307		9	11	79	
DIRIDECH	2571	1316		9	12	86	
DLGVNCEK	2572	2617	1 0144	9	13	93	0 0002
DLVIVRH	2573	1134		8	12	86	
DVIVRRR	2574	1143		8	11	79	
EGTALCAWY	2575	1524		10	11	79	
EGVWMMNR	2576	1915	24 0077	9	14	100	0 0014
EMGQNTIR	2577	2345		8	12	86	
EVFVCEK	2578	2596	1090 24	9	12	86	0 0170
FLVFTKGLH	2579	2598		10	11	79	
FOVFTKGLPR	2580	2598		11	11	79	

Sequence	Length (AAs)	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*11101
FGAYMSKAH	2581	1269		9	12	86	
FGYCAKQVR	2582	2554	1 0960	9	12	86	0.0005
FLILADAG	2583	728		8	14	100	
FLFAMTHY	2584	2792		8	14	100	
FLGLTHDAH	2585	1567		10	13	93	
GAARALAH	2586	146		8	11	79	
GAARALAHGVR	2587	146		11	11	79	
GAUCWMPER	2588	1916		8	14	100	
GAYMSKAH	2589	1270		8	12	86	
GAELMAY	2590	129		8	13	93	
GFAYMSK	2591	1268		8	12	86	
GFAYMSKAH	2592	1268		10	12	86	
GFYKQVR	2593	2645		9	11	79	
GGARALAH	2594	145		9	11	79	
GGSGAY	2595	1308		8	11	79	
GGKAGVY	2596	26		10	14	100	
GGKAGVY	2597	27		9	14	100	
GGRIIFCI	2598	1392	24 0078	9	14	100	0.0001
GGRIIFCSK	2599	1392		11	14	100	
GGVLAAAY	2600	1669		10	12	86	
GGVILPR	2601	32		8	13	93	
GGVILPRR	2602	32	24 0080	9	13	93	0.0010
GYILPNR	2603	3037		8	11	79	
GLPVXXH	2604	1552		8	13	93	
GLPVSAAR	2605	1004		8	11	79	
GLSAFLH	2606	2921		8	11	79	
GLSAFLHSY	2607	2921	1073 03	10	11	79	0.0005
GLTHDAH	2608	1569		8	13	93	
GNHVSPTH	2609	1931		8	12	86	
GNHVSPTH	2610	1931		9	12	86	
GNIRVEFNK	2611	2248		11	12	86	
GSSDLVIVR	2612	1131		10	12	86	
GSSDLVIVRH	2613	1131		11	12	86	
GSSGFGY	2614	2641		8	11	79	
GTFPINAY	2615	2063		8	11	79	
GVAGAVAK	2616	1863	1073 10	10	12	86	1.4000
GVCTVYH	2617	1081		8	11	79	
GVGVILPNR	2618	3035	1090 25	10	11	79	0.0140
GVLAALAAAY	2619	1670	1174 19	9	12	86	0.0110
GVRAIKTISR	2620	45		11	11	79	
GVRCFKALY	2621	2619		11	14	100	
GVRLDGNY	2622	154		11	12	86	
GVVCAALIR	2623	1900		9	11	79	
GVVCAALIRH	2624	1900		10	11	79	
GVVCAALIRH	2625	1900		11	11	79	

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101
GWYLLPRH	2626	33		8	13	93	
GWYLLPRGPR	2627	33		11	13	93	
HAQVIPVR	2628	1141		8	11	79	
HAQVIVRR	2629	1141		9	11	79	
HAQVIVRRH	2630	1141		10	11	79	
HAPTGSCK	2631	1234		8	14	100	
HAPTGSCKSTK	2632	1234		11	13	93	
HCLSAFSLH	2633	2920		9	11	79	
HCLSAFSLHSY	2634	2920		11	11	79	
HCPTEPLY	2635	1624		8	11	79	
HCPTEPLYR	2636	1624		9	11	79	
HIDAHLSQIK	2637	1572		11	14	100	
HLHAPTGSCK	2638	1232	1073 16	10	12	86	0 0024
HLHQNIVDQY	2639	696		11	11	79	
HLIFCHSK	2640	1395		8	14	100	
HLIFCHSPF	2641	1306	1090 26	9	14	100	0 0006
HLIFCHSPFF	2642	1395	1073 12	10	14	100	0 0002
HMWNFSGQY	2643	1769		11	13	93	
HSYSPGENR	2644	2928		10	11	79	
HTPGVPCVR	2645	222	1 1061	10	11	79	0 0012
IACASGNIH	2646	1925	24 0079	9	14	100	0 0003
IDAHLSQIK	2647	1573		10	14	100	
IFCHSKKK	2648	1397		8	14	100	
IICDECH	2649	1317		8	12	86	
ININGSWH	2650	415		8	11	79	
ITRVESENK	2651	2250	1 0137	9	12	86	0 0079
ITASTGK	2652	1296		8	12	86	
IVDGYLY	2653	701		8	12	86	
IVPDGVH	2654	2613		9	11	79	
IVGGVYLLPR	2655	30	1 0962	10	13	93	0 0044
IVGGVYLLPHR	2656	30	1 1060	11	13	93	0 0056
KCELAALK	2657	1404		8	12	86	
KFATGAKDVH	2658	2553		10	12	86	
KGGHHLFCH	2659	1391		10	11	79	
KGLHKPAH	2660	2604		8	11	79	
KLGVPPLR	2661	2944		8	12	86	
KNEVGVJEF	2662	2594		11	11	79	
KSTKVPAAV	2663	1241	13 0016	9	12	86	0 0001
KTKRNTIR	2664	10		8	12	86	
KTPRNTIRH	2665	19	24 0085	9	12	86	0 0100
KTSRHYJPR	2666	51	1 0952	9	11	93	0 0640
KTSRQFRGR	2667	51		11	12	86	
LADYVSSJAY	2668	1305		11	11	79	
LAQFPGK	2669	1729		8	12	86	
LDOAETAGAR	2670	1338		10	12	86	

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*11101
LELLADAR	2671	727		9	12	100	
LEFSRRH	2672	290		8	11	79	
LEFGAMSK	2673	1267	24 0086	9	12	86	0.2900
LEFGATSKAH	2674			11	12	86	
LEGAARALAH	2675	144		10	11	79	
LEGRATRK	2676	44		8	12	86	
LEGVVEK	2677	2618		8	12	100	
LEIAAGGHH	2678	1924		10	14	100	
LEANLWR	2679	2235	1 0959	9	12	86	0.0005
LEFESKK	2680	1396		8	14	100	
LEFESKK	2681	1396	1 0123	9	14	100	0.1900
LEINEASH	2682	414		9	11	79	
LEFPGVR	2683	2612	1 1066	10	11	79	0.0001
LEAFHAY	2684	1030		8	14	100	
LELLADAR	2685	726	1090 28	10	14	100	
LEFRGFR	2686	36		8	13	93	
LEFRGSR	2687	97		8	12	86	
LESAFSLHSY	2688	2922		9	11	79	0.0002
LESLRHH	2689	2479	13 0019	8	12	86	
LEKSLRHH	2690	2479	24 0087	9	12	86	0.0001
LESLRHH	2691	690		9	12	86	
LEGFALMGY	2692	126		11	12	86	
LESLTDPFH	2693	2176		10	13	93	
LEVAYQATVCAR	2694	1591		11	11	79	
LEVLAGY	2695	1853		8	11	79	
MEFSYDR	2696	2668		8	11	79	
MESSGFQI	2697	2640		9	11	79	
MNRLAFASR	2698	1921		10	14	100	
MNLTGFK	2699	558		8	11	79	
MSINFKPOR	2700	1		9	11	79	
MSINFKFQK	2701	1		10	11	79	
NGGFRGR	2702	2726		8	11	79	
NGSLRPH	2703	305		8	11	79	
NFISGIGY	2704	1772		8	14	100	
NGVQWTVY	2705	1080		8	11	79	
NGVQWTVH	2706	1080		9	11	79	
NHVFSENK	2707	2249	1 0498	10	12	86	0.0062
NVLVQHLT	2708	709	1073 01	9	12	86	0.0140
NHRRKQGVK	2709	14	2 0168	10	11	79	0.0007
NHFGPVQDDH	2710	1549		11	13	93	
PALSTGLH	2711	688		9	12	86	
PALSTGLHH	2712	688		11	12	86	
PGCSWLR	2713	1976		8	11	79	
PGTGLSSDLY	2714	1127		10	11	79	
PQLGRVCEK	2715	2616		10	13	93	

Sequence	SeqId Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*11101
PLGVKVR	2716	224		8	12	86	
PLGVAVWMT	2717	1913		11	13	93	
PLGVAVKGV	2718	25		11	14	100	
PLGVVQHH	2719	1551		9	13	93	
PLGVWLY	2720	79		8	14	100	
PLVSLYCK	2721	1295		9	11	79	
PLVGAARALAH	2722	143		11	11	79	
PLVPSYDTR	2723	2667		9	11	79	
PLVILGVR	2724	1281		8	13	93	
PLVAVVGLTDR	2725	514		11	13	93	
PLVIXMK	2726	1607		8	11	79	
PLVFLKH	2727	587		8	13	93	
PLVRRSR	2728	109	1 0954	9	12	86	0 0005
PLVSLKSLK	2729	1236	1 0121	9	13	93	0 0001
PLVHAPPLY	2730	1621		11	11	79	
PLVVGITDR	2731	516	1 0956	9	13	93	0 0005
QALTAGAR	2732	1340		8	12	86	
QVGVTLER	2733	29		11	13	93	
QLFTSEPR	2734	289		8	12	86	
QLFTSPRR	2735	289	1 0955	9	11	79	0 0330
QLTAPSLK	2736	2210		8	11	79	
QVNDQV	2737	699		8	11	79	
QVNDVQVLY	2738	699		10	11	79	
RAAVLTGVAK	2739	1186		11	11	79	
RAAHGVR	2740	149		8	14	100	
RAHKTSEI	2741	47		9	11	79	
RAHNVSPTH	2742	1930	24 0088	9	12	86	0 0001
RAHNVSPTH	2743	1930	24 0105	10	12	86	0 0001
RAHVGVR	2744	40		8	13	93	
RAHVGVRATR	2745	40		11	11	79	
RAHRRDPK	2746	59	24 0081	9	13	93	0 0017
RAHSLSPR	2747	1154		8	12	86	
RAHGVRAIR	2748	43		8	11	79	
RAHGVRAIRK	2749	43	1073 11	8	11	79	0 0290
RAHLSATSLH	2750	2918		11	11	79	
RAHLSR	2751	1923		8	14	100	
RAHLSRGNH	2752	1923		11	12	100	
RAHFDLQVR	2753	2611	1174 18	11	11	79	0 0270
RAHPTAY	2754	1029		9	12	86	
RAHVGVEH	2755	635		9	14	100	
RAHVGVEHR	2756	635	1073 13	10	14	100	0 0200
RAHRRPQDK	2757	13		11	11	79	
RAHRRPR	2758	55		8	13	93	
RAHKKMALY	2759	2621	1174 21	9	14	100	0 5000
RAHEDVNY	2760	156	1174 17	9	12	86	0 0068

Sequence	Seq ID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101
SAPGLHSY	2761	2923		8	11	79	
SAPGLSAPSEK	2762	2707		11	11	79	
SLSSNVSAH	2763	2818		10	12	86	
SLSLVIVTR	2764	1133		8	12	86	
SLSLVIVTRH	2765	1133		9	12	86	
SLKSLKVPAAAY	2766	1239		11	12	86	
SMILTPSA	2767	2178		8	14	100	
SARSLEHH	2768	2480		8	12	86	
SSSLVIVTR	2769	1132	24 0089	9	12	86	0 0044
SSSLVIVTRH	2770	1132	24 0106	10	12	86	0 0013
SSNVSAH	2771	2820		8	12	86	
SLGLHH	2772	691		8	12	86	
SLKGLAAY	2773	1242		8	12	86	
SINPKPKR	2774	?		8	11	79	
SINPKPKRK	2775	?		9	11	79	
SINPKPKRKTK	2776	?		11	11	79	
SVAALLGAY	2777	1262		11	14	100	
LCGLALMGY	2778	127		10	13	93	
LCGLSSDLY	2779	1129		8	11	79	
LCGLRHSR	2780	110		8	12	86	
LCGLFYCK	2781	1375		9	11	79	
LCGLTHDAH	2782	1568	24 0082	9	13	93	0 0001
LCGLSKSTK	2783	1237		8	13	93	
LCGLAYMSK	2784	1266	1073 14	10	12	86	0 0610
LCGLFIPLLY	2785	1622	1073 04	10	11	79	0 0007
LCGLGTPLYH	2786	1622		11	11	79	
LCGLSLGLIH	2787	686		11	11	79	
LCGLWARMILMTH	2788	2871		11	11	79	
LCGLPKRK	2789	3		8	11	79	
LCGLPKRTPK	2790	3		10	11	79	
LCGLGTPRTPR	2791	3		11	11	79	
LCGLRQGVK	2792	15		9	11	79	
LCGLSSNVSAH	2793	2817		11	12	86	
LCGLRSQPR	2794	52		8	13	93	
LCGLRSQPRGR	2795	52	24 0107	10	12	86	0 0001
LCGLRSQPRGRH	2796	52		11	12	86	
LCGLTGROK	2797	1050		8	12	86	
LCGLTPPSH	2798	2177	24 0083	9	13	93	0 0001
VAAALLGAY	2799	1263		10	14	100	
VAGALVAFK	2800	1864	24 0090	9	12	86	0 8930
VATVALVCAH	2801	1592	1 1064	10	11	79	0 0038
VCAALLER	2802	1902		8	11	79	
VLAALLHH	2803	1902		9	11	79	
VCEKAAALY	2804	2622		8	14	100	
VCTRGVAK	2805	1189		8	11	79	

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101
VLPYRWH	2806	614		9	13	93	
VLSYRHHWHY	2807	614		10	13	93	
VLCVRRK	2808	2597		8	12	86	
VLCVFRKGR	2809	2597		11	11	79	
VFLCGVR	2810	2614		8	11	79	
VFLTHDAH	2811	1566		11	13	93	
VGLVLAALAAV	2812	1668	24 0084	11	12	86	0 0019
VGLVYLFR	2813	31		9	13	93	
VGLVYLFR	2814	31		10	13	93	
VGLVYLFR	2815	3036	F104 01	9	11	79	0 0100
VGLVLAALR	2816	1899		10	11	79	
VGLVLAALR	2817	1899		11	11	79	
VLAALAAV	2818	1671		8	12	86	
VLDQAEIAGAR	2819	1337		11	12	86	
VLEKVVV	2820	157		8	12	86	
VLSMLTDPSSH	2821	2175		11	13	93	
VLDLAGY	2822	1852		9	11	79	
VMLSSYGFQY	2823	2639		10	10	79	
VTRHADVIPVR	2824	1138		11	11	79	
VVCAALR	2825	1901		8	11	79	
VVCAALRR	2826	1901		9	11	79	
VVCAALRRH	2827	1901		10	11	79	
VVCAALRR	2828	1898		11	11	79	
VVGGTDR	2829	517		8	13	93	
WAGWLLSPR	2830	93		9	12	86	
WAGFGTPWPI	2831	76		11	12	86	
WARMILMH	2832	2873		9	12	86	
WGPTDPRR	2833	107		8	12	86	
WGPTDPRR	2834	107		9	12	86	
WGPTDPRRSH	2835	107		11	12	86	0 0005
WLSFRGSR	2836	96	1 0953	9	12	86	
WMNRILAFASR	2837	1920		11	14	100	0 0810
WMNSTGFIR	2838	557	1174 16	9	11	79	
WNFSGDY	2839	1771		9	14	100	
YDAGCAWY	2840	1526		8	11	79	
YDMLTECH	2841	1315		10	12	86	
YGLQSPQAR	2842	2644		10	11	79	
YLPFRGFR	2843	35	1 0951	9	13	93	0 0005
YSPGFRR	2844	2930		8	11	79	
YVAVRFR	2845	637		8	14	100	
YVFESDAAR	2846	1939	1 1065	10	12	86	0 0001

Table XVIII

HCV A24 Motif with Binding Information

Table XVIII HCV A24 Motif With Binding Information

Frequency	Peptide	Isolated	Position	Sequence	SeqID Num	A*2401	Motif
86			319	AWDMMNW	2847		A241
79			1248	AYAGGYKVL	2848		A241
100	13 0132		1421	AYRGLDVSVI	2849	0 0009	A241
79			1525	CYDAGCAW	2850		A241
79			1525	CYDAGCAWYEL	2851		A241
100			1468	DFSLOPIF	2852		A241
100			1468	DFSLOPIFI	2853		A241
86		1996	1765	FWAKHMMWIF	2854	6 9000	A241
86	24 0092		1765	FWAKHMMWIF	2855		A241
93			129	GFADLMGYI	2856		A241
79			129	GFADLMGYPL	2857		A241
79			2669	GFSYDTRCF	2858		A241
79			1027	GWRLAPI	2859		A241
86	13 0133		1859	GYGAGVAGAL	2860	0 0003	A241
79	13 0131		135	GYPLVGAFL	2861	0 0057	A241
86			2728	GYRCRASGVL	2862		A241
93	1174 08	1996	1769	HMMNFISGI	2863		A241
86			176	IFLLALLSCL	2864		A241
86			2591	IMAKNEVF	2865		A241
93			23	KPGGGGI	2866		A241
86			1813	LTNLGGW	2867		A241
86			2872	LWARMILMTHF	2868		A241
86			2241	LWRJEMGGII	2869		A241
79			1135	LYLVTRHADVI	2870		A241
100			1770	MWNFISGI	2871		A241
100			1770	MWNFISGIQYL	2872		A241
93	1073 18	1993	636	MYVGGVEHRL	2873	0 0270	A241
100	24 0091	1996	1772	HFISGIQYL	2874	0 0170	A241
79			2667	PMGFSYDTRCF	2875		A241
86			1732	QFKOKALGL	2876		A241
86			1732	QFKOKALGLL	2877		A241
100			1919	QWNNRLIAF	2878		A241
100	13 0075	1995	1778	QYLALSLT	2879	0 0480	A241
79	13 0134	1995	2647	QYSPGQVVEF	2880	0 0180	A241
79			2647	QYSPGQVVEFL	2881		A241
86			317	RMADMMMNW	2882		A241
86			2875	RMILMTHF	2883		A241
86			2875	RMILMTHFF	2884		A241
93			635	RMVVGVEHLL	2885		A241
100			173	SFSIFLLAL	2886		A241
100	24 0108		173	SFSIFLLAL	2887	0 0041	A241
100	1174 10		2178	SMILTPSHI	2888		A241
79			1608	SWDMMKCL	2889		A241
86			1164	SYLKGSSGGPL	2890		A241
79			556	TWNINSTGF	2891		A241

Conservation	freq	Peptide	Filed	Position	Sequence	SeqID Num	A*2401	Motif
86	12			1664	TWLVGGVL	2892		A241
93	13			1297	TSIRGKF	2893		A241
86	12		1995	1297	TSIRGKEL	2894	0.0230	A241
93	13	13.0074		1566	VETGLHI	2895		A241
79	11			2649	VMSSVGF	2896		A241
93	13	1073.19	1993	34	VYLLFRGPR	2897	0.0016	A241
100	14			1920	WMRLIAF	2898		A241
100	14			1422	YYRGLDVSII	2899		A241

Table XIXa HCV DR-Super Motif Binding Data Not Included

Core Sequence	Core SeqID Num	Core Freq.	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position in Poly-protein	Peptide No.	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
FGAYMSKAI	3052	12	86	TLGFGAYMSKAIIGVD	2900	1266		5	36
FGCTWNNSF	3053	12	86	GNWFGCTWNMSGTFT	2901	550	1283.13	11	79
FKQKALGLL	3054	12	86	AEQFKQKALGLLQTA	2902	1730	1283.35	12	86
FTLALLSCL	3055	12	86	FSIFLLALLSCLTVP	2903	174		6	43
FPIDIGRVVC	3056	11	79	LIVFPDILGVRVCFKRM	2904	2612		11	79
FQVAIHJHAP	3057	12	86	PQTFQVAIHJHAPTGS	2905	1225	1283.19	6	43
FRAAYCTRG	3058	12	86	VGFRAAYCTRGVAK	2906	1182		7	50
FSHLLALL	3059	14	100	GCFSFSIFLALLSCL	2907	171	1283.09	12	86
FSIDPFTFI	3060	14	100	IVDFSLDPFTFIEFT	2908	1466	1283.28	11	79
FTEAMTRYG	3061	14	100	LRVFTEAMTRYSAAP	2909	2789		7	50
FIPSPVAVG	3062	13	93	VYCFIPSPVAVGTTD	2910	509	1283.12	13	93
FTHPALST	3063	11	79	PCSFTHPALSTGLJ	2911	681		9	64
FWAKHMAWNE	3064	12	86	LEVFWAKHMAWNEISG	2912	1762		3	21
HDALHLSQT	3065	14	100	LTHIDAHFLSQTQQA	2913	1570		7	50
HDNCTCTQ	3066	12	86	DSWIDCNTCTVTQVD	2914	1454	1283.27	12	86
HDLLFCGEA	3067	12	86	GKVIDLTCGEADLM	2915	120		12	86
HEANLLWRQ	3068	12	86	ADLJEANLLWRQEMG	2916	2233		7	50
HEHALLSC	3069	14	100	SFSIFLALLSCLTV	2917	173		6	43
ILGGWVAAQ	3070	12	86	LENILGGWVAAQLAP	2918	1813		8	57
ILGIGFVLD	3071	12	86	STHIGIGFVLDQAE	2919	1328		8	57
ILRPHVGGPG	3072	11	79	CAAHILRPHVGGPGGA	2920	1903	1283.42	11	79
ILSPGALVV	3073	13	93	LPAILSPGALVVGAV	2921	1888		11	79
INAYTLGPG	3074	12	86	TFPINAYTLGPGTIPS	2922	2064		8	57
IPLVGAPLG	3075	11	79	MGYIPLVGAPLGGAA	2923	134		10	71
IRVSENRK	3076	12	86	GGNITRVSENRKVVI	2924	2247		10	71
ITSCSSNVG	3077	14	100	LELITSCSSNVSAIH	2925	2813	1283.57	11	79
IIVFDIGVR	3078	11	79	ARTIIVFPDILGVRVCF	2926	2610	1283.52	11	79
LAALAAAYCL	3079	12	86	GGVLAALAAAYCLTTG	2927	1669		8	57
LADGGGSGG	3080	11	79	GKFLADGGGSGGAYD	2928	1302		10	71
LAGLSTLPG	3081	14	100	IOYLAGHSTLPGNPA	2929	1777	1283.37	14	100
LAGYGAGVA	3082	11	79	VDILAGYGAGVAGAL	2930	1854		10	71
LATAFPYGS	3083	12	86	LVVLATATPPGSAIV	2931	1348		9	64
LDPFTFIEF	3084	12	86	DFSLDPTFFIETTV	2932	1468		5	36
LDQAFIAGA	3085	12	86	GTVLDQAFIAGARLV	2933	1335	1283.23	12	86

Table XIXa HCV DR-Super Motif Binding Data Not Included

Core Sequence	Core SeqID Num	Core Freq	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position In HCV Poly-protein	Peptide No.	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
LEHLSGSS	3086	13	93	EYDELELTSCSSNV	2934	2810		13	93
LEVVLSTWV	3087	12	86	SADLEVVTSTWVLVG	2935	1655		11	79
LEFLADAR	3088	14	100	VVLLFLLADARVCS	2936	724	1283.15	4	29
LGGWVAAQL	3089	12	86	FNILGGWVAAQLAPP	2937	1814		8	57
LGIGTVLDQ	3090	13	93	TTILGIGTVLDQAET	2938	1329		9	64
LGVRALRKL	3091	12	86	GPRLGVRALRKTSE	2939	41		10	71
LGVRVCEKM	3092	14	100	FPDLGVRVCEKMALY	2940	2615	1283.53	11	79
LHGLSAFSL	3093	11	79	IERLHGLSAFSLHSY	2941	2916		6	43
LHGPTPLY	3094	11	79	KPTLHGPTPLYRLG	2942	1620	1283.32	11	79
LHQNIQDVQ	3095	12	86	LIHLHQNIQDVQYLY	2943	694		10	71
LHSYSPGL	3096	11	79	AFSLHSYSPGEINRV	2944	2924	1283.60	11	79
LIAFASRGN	3097	14	100	MNRLIAFASRGNHVS	2945	1921	1283.44	12	86
LILANLWR	3098	12	86	DADLIEANLWRQFM	2946	2232	1283.47	7	50
LHCHSKKK	3099	14	100	GRHLHCHSKKKCDE	2947	1393	1283.25	14	100
LIHSCSSNV	3100	14	100	DLELITSCSSNVSA	2948	2812		13	93
LLALLSCLT	3101	12	86	SIFLLALLSCLTTPA	2949	175		5	36
LEFLFLADA	3102	14	100	YVVLFLFLADARVC	2950	723		5	36
LEFNILGGW	3103	12	86	QNTTLEFNILGGWVAA	2951	1809		4	29
LLADARVC	3104	13	93	LLFLLADARVCACL	2952	726		9	64
LPAILSPG	3105	13	93	LVNLLPAILSPGALV	2953	1884		10	71
LMGYIPLVAG	3106	11	79	FADLMGYIPLVGAFL	2954	130		11	79
LNPSVAATL	3107	14	100	VLVLNPSVAATLGFG	2955	1256	1283.22	14	100
LPAILSPGA	3108	13	93	VNLLPAILSPGALVV	2956	885		11	79
LPALSTGLI	3109	12	86	FTTLPALSTGLIHJH	2957	684	1283.14	11	79
LPRGPRIG	3110	13	93	VYLLPRGPRIGVRA	2958	34	1283.02	13	93
LRDIAVAVE	3111	11	79	HNGLRDIAVAVEPVV	2959	966		4	29
LPRTGVPPI	3112	12	86	ASCLRLKLGVPPLRVW	2960	2939	1283.61	7	50
LSAFSLHSY	3113	11	79	LHGLSAFSLHSYSPG	2961	2919	1283.59	11	79
LSAFSLKAI	3114	11	79	ASQLSAFSLKATCTT	2962	2208	1283.46	7	50
LSNLSLRHH	3115	12	86	INALSNLSLRHHNMV	2963	2476		4	29
LSPGALVVG	3116	13	93	PAILSPGALVVGVC	2964	1889		11	79
LSPILSTI	3117	11	79	RSFISPIILSTTEWQ	2965	664		7	50
LSPRGRPS	3118	11	79	GWLLSPRGRPSWGP	2966	95		11	79
LSLGLIHJH	3119	12	86	LPALSTGLIHJHJH	2967	687		10	71

Table XIXa HCV DR-Super Motif Binding Data Not Included

Core Sequence	Core SeqID Num	Core Freq.	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position In HCV Poly-protein	Peptide No.	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
LTGGEADLM	3120	12	86	IDTLTCGEADIMGYI	2968	123	1283.05	12	86
LTHDAHFL	3121	13	93	FTGLTHDAHFLSQF	2969	1567	1283.30	13	93
LTSMHTDPS	3122	13	93	VAVLTSMHTDPSHIT	2970	2173		9	64
LVAAYQATVC	3123	12	86	FPYLVAYQATVCARA	2971	1588		9	64
LVDILAGYGG	3124	11	79	GKVLVDILAGYGGAV	2972	1850		9	64
LXGGVLAAL	3125	12	86	TWVLXGGVLAALAAAY	2973	1664	1283.34	12	86
LVLNPSVAA	3126	14	100	YKVLVLPNSVAATLIG	2974	1254		14	100
LVLNLPAIL	3127	11	79	TEDLVNLPAILSPG	2975	1881		10	71
LVTIRHADV	3128	11	79	DLVLTIRHADVIVPR	2976	1134	1283.17	11	79
LVAAGVCAA	3129	11	79	PGALVVAAGVCAAILR	2977	1894		11	79
LVLALATAP	3130	12	86	GARLVVLATATPPGS	2978	1345	1283.24	11	79
LWARMILMT	3131	12	86	APTLWARMILMTIHF	2979	2869		11	79
LWQJENGGN	3132	12	86	ANLLWQJENGGNITR	2980	2238	1283.48	12	86
LYRI GAVON	3133	11	79	TPLLRYLGAVQNEVT	2981	1627		9	64
MAENEVECV	3134	12	86	THMAKNEVECVQPE	2982	2389	1283.51	9	64
MAWDMMINSW	3135	12	86	GHRMAWDMMINWSPT	2983	315	1283.10	12	86
MGGNTRVE	3136	12	86	RQEMGGNTRVESEN	2984	2243	1283.49	12	86
MGYIPLVGA	3137	11	79	ADLMGYIPLVGAPLG	2985	131	1283.06	11	79
MLTDPSHIT	3138	14	100	LTSMLTDPSHITAET	2986	2176	1283.45	8	57
MNRI LAEAS	3139	14	100	VQWMNRLIAEASRGN	2987	1918		14	100
MTRYSAAPG	3140	14	100	TEAMTRYSAAPGDPP	2988	2793		10	71
MWNFSGIQ	3141	14	100	AKHMWNFISGQYLA	2989	1767	1283.36	12	86
MYVGGVPHR	3142	14	100	KVRMYVGGVEHRLNA	2990	633		5	36
VAGALVAFK	3143	12	86	GAGVAGALVAFKVMS	2991	1861		7	50
VAHLIAPITG	3144	12	86	TFQVAHLIAPITGSGK	2992	1227		6	43
VATDALMTG	3145	12	86	VVVVATDALMTGYTG	2993	1437	35.0106	6	43
VAYQATVCA	3146	12	86	PYLVAYQATVCAAAQ	2994	1589		11	79
VCAALRRH	3147	11	79	VGVVCAALRRHIVGP	2995	1899		10	71
VCEKMALYD	3148	14	100	GVRVCEKMALYDVVS	2996	2619	1283.54	11	79
VCCDHLEFW	3149	12	86	GLPYCCDHLEFWESV	2997	1552	35.0109	6	43
VCTRGVAKA	3150	11	79	RAAVCTRGVAKAVDF	2998	1186	1283.18	11	79
VTCVQPEKG	3151	12	86	KNEVFCVQPEKGGRE	2999	2594		10	71
VFTDNSSPP	3152	11	79	RSPIVFTDNSSPPAVP	3000	1211		10	71
VFGLTHHD	3153	13	93	WESVFTGLTHHDHIF	3001	1563	1283.29	6	43

Table XIXa HCV DR-Super Motif Binding Data Not Included

Core Sequence	Core SeqID Num	Core Freq	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position In HCV Poly-protein	Peptide No.	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
VGGVLAALA	3154	12	86	WVLVGGVLAALAAAYC	3002	1665		12	86
VGGVYLLPR	3155	13	93	GQIVGGVYLLPRRGP	3003	28		13	93
VGSQLPCEP	3156	12	86	QYLVSQLPCEPEPD	3004	2158		6	43
VGVVCAAIL	3157	11	79	ALVGVVCAAILRRH	3005	1896		11	79
VIDNCVCT	3158	12	86	FDSVIDNCVCTQIV	3006	1453		12	86
VIDLTCGF	3159	12	86	LGGVIDTLTCGFADL	3007	119	1283 04	11	79
VLAALAAAYC	3160	12	86	VGGVLAALAAAYCLTT	3008	1668		8	57
VLATAIPPG	3161	13	93	RLVLATAIPPGSVT	3009	1347		9	64
VLEDGVNYA	3162	12	86	GVRVLEDGVNYATGN	3010	154	1283 07	12	86
VLNPSVAAT	3163	14	100	KVLVLNPSVAATLGF	3011	1255		14	100
VLTSMTDP	3164	13	93	DVAVLTSMTDPSSH	3012	2172		9	64
VLTSCTGNT	3165	11	79	ASGVLTSCTGNTLTC	3013	2734		10	71
VLVDILAGY	3166	11	79	LGGVLVDILAGYGAG	3014	1849		10	71
VLVGGVLAAL	3167	12	86	STWVLVGGVLAALAA	3015	1663		12	86
VLVLNPSVA	3168	14	100	GYKVLVLNPSVAATL	3016	1253	1283 21	14	100
VNLLPAILS	3169	12	86	EDLVNLLPAILSPGA	3017	1882	1283 39	11	79
VPESDAAAR	3170	12	86	THYVPESDAAARVTQ	3018	1937		7	50
VSTAWVVG	3171	12	86	LEVVTSTWVLVGGVL	3019	1658	1283 33	12	86
VVAIDALMT	3172	11	79	DVVVVAIDALMTGYT	3020	1436	1283 26	6	43
VVC AAILRR	3173	11	79	VGVVVC AAILRRHVG	3021	1898		10	71
VGVVVC AAI	3174	11	79	GALVVGVVVC AAILRR	3022	1895	1283 41	11	79
VVLATAIPP	3175	12	86	ARLVVLATAIPPGSV	3023	1346		9	64
VYCTIPSPV	3176	13	93	CGPVYCTIPSPVVVG	3024	506	1283 11	13	93
WAGWTLSPR	3177	12	86	GGGWAGWTLSPRGR	3025	90		5	36
WARMHMTIH	3178	12	86	PTLWARMHMTIHFS	3026	2870	1283 58	11	79
WGADTAACG	3179	12	86	ITWGDATACGDII	3027	988		6	43
WGPDPRRR	3180	12	86	RPSWGPDPRRRSRN	3028	104		10	71
WMNRLIAFA	3181	14	100	AVQWMNRLIAFASRG	3029	1917	1283 43	14	100
WRLLAPITA	3182	11	79	SKGWRLIAPITAYAQ	3030	1025	1283 16	4	29
WIGALLIPC	3183	11	79	SYTWIGALLIPTCAAE	3031	2456	1283 50	9	64
WYFLIPAFI	3184	12	86	GCAWYFLIPAEITVR	3032	1529		5	36
YALGNLPGC	3185	12	86	GVNYATGNLPGCSFS	3033	161	1283 08	11	79
YCFIPSPVV	3186	13	93	GPVYCFIPSPVVVGT	3034	507		13	93
YDAGCAWYF	3187	11	79	CECYDAGCAWYELTP	3035	1523		10	71

Table XIXa HCV DR-Super Motif Binding Data Not Included

Core Sequence	Core SeqID Num	Core Freq	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position In HCV Poly-protein	Peptide No.	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
YDIHCDIC	3188	12	86	GGAYDIIICDECHST	3036	1312		10	71
YDIETITSC	3189	13	93	QPEYDLELITSCSN	3037	2808	1283.56	11	79
YGAGVAGAL	3190	12	86	LAGYGAGVAGALVAF	3038	1857	1283.38	11	79
YGHQYSPGQ	3191	11	79	GSSYGFQYSPGQVE	3039	2641	1283.55	10	71
YGFHLDGCG	3192	11	79	YSTYGFHLDGCGSG	3040	1298		10	71
YKVLVLNPS	3193	14	100	AQGYKVLVLNPSVAA	3041	1251	1283.20	11	79
YLAGLSLIP	3194	14	100	GIQVLAGLSLIPGNP	3042	1776		14	100
YLGSSGGRP	3195	12	86	PVSYLKSSSGGPLLC	3043	1162		6	43
YLRDPTTP	3196	11	79	RVVYI TRDPTTPI AR	3044	2833		9	64
YQATVCARA	3197	13	93	LVAYQATVCARAQAP	3045	1591		11	79
YRGLDVSVI	3198	14	100	VAYYRGLDVSVIPTS	3046	1420		7	50
YRLGAVQNE	3199	11	79	PLLYRLGAVQNEVTL	3047	1628		9	64
YRRCRASGV	3200	13	93	NCGYRRCRASGVLT	3048	2726		10	71
YSHEPLDLP	3201	11	79	GACYSHEPLDLPQII	3049	2902		6	43
YSPGFNRV	3202	11	79	LHSYSPGFNRVASC	3050	2927		8	57
YVGHICGSV	3203	12	86	SAMYVGDLCGSVFLV	3051	273	35.0103	8	57
VGHYLLPNR	3204	11	79			3036	080.02		

Table XXa HCV DR 3A Motif Binding Data Not Included

Core Sequence	Core SeqID Num	Core Freq	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position In H ₁ V Poly-protein	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
HLADGGSG	3205	11	79	YGRFLADGGGCGAY	3224	1301	10	71
ESLDPTFTT	3206	14	100	TVDFSLDPTFTFTT	3225	1466	11	79
LEGFPGDD	3207	14	100	MPFLGEGPGDDLSL	3226	2401	11	79
LPGLPFDV	3208	12	86	GSGLPCEPFDVAVL	3227	2162	9	64
MAWDMMMSW	3209	12	86	GHRMAWDMMSWSP	3228	315	12	86
MLTDSHLL	3210	14	100	LTSMLTDSHLLTET	3229	2176	8	57
MSADLEAVT	3211	11	79	MACMSADLEAVTSTW	3230	1651	6	43
VAEDALMIG	3212	12	86	VVVVATDALMTGYTG	3231	1417	6	43
ACQDHLFTW	3213	12	86	GLPVCQDHLFFWESV	3232	1552	6	43
VFPHLCARV	3214	11	79	RLVFPDLGVRCVK	3233	2611	11	79
VFIDNSSP	3215	11	79	RSPVFIDNSSPAVP	3234	1211	10	71
VLCYCVDG	3216	13	93	DSSVLCGYDAGCAW	3235	1518	10	71
VFEDGNYA	3217	12	86	GVRVLEDGNYATGN	3236	154	12	86
VLADLAGV	3218	11	79	LGRVLADLAGYGAG	3237	1849	10	71
VQPEKGGRK	3219	11	79	VFCVQPEKGGKKPAR	3238	2597	11	79
YDIETITSC	3220	13	93	QPFYDIETITSCSSN	3239	2808	11	79
YSHPIDLP	3221	11	79	GACYSHPIDLPQII	3240	2902	6	43
YVGDLCGV	3222	12	86	SAMVVGDLCSVFLV	3241	273	8	57
YVHSIDAAA	3223	12	86	PTHYVPESDAAARVT	3242	1936	12	86

Table XXc HCV 3B Motif

Core Sequence	Core SeqID Num	Core Freq	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position In HCV Poly protein	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
ECISEKKCD	3243	14	100	HLIFCHSKKKCDELA	3250	1395	14	100
ESYDTRCED	3244	11	79	PMGTSYDTRCFDSTV	3251	2667	11	79
LAFLQKQKA	3245	12	86	GMQLAEQFKQKALGL	3252	1726	8	57
LKPTLHGPT	3246	11	79	LIRLKPILLHGPTPLL	3253	1616	10	71
VRATRKISE	3247	11	79	RLGVRATRKISTERSQ	3254	43	10	71
YIVLRIADV	3248	12	86	SDLVLVTRIADVIPV	3255	1133	11	79
MSLSNPKPQR	3249		79			1		

HCV 3B Motif Binding Data

Table XXd

[illegible]

Table XXII
HCV Analogs

AA	Sequence	SeqID Num	Fixed Nomen	A1 Motif	A2 Super Motif	A3 Super Motif	A24 Motif	R7 Super Motif	1 Anchor Fixer
9	RVXKMLY	3642		N	N	Y	N	N	No
9	AVXTHGVAK	3643		N	N	Y	N	N	
9	LVXVQPER	3644		N	N	Y	N	N	
9	HLIFVHSPK	3645		N	N	Y	N	N	
9	LPXSF SIF	3646		N	N	Y	N	Y	
9	LPXHSKK	3647		N	N	Y	N	N	
10	VLAALAAAYX	3648		N	Y	N	N	N	
10	HLIFVHSPK	3649		N	N	Y	N	N	
10	AAXNWTRGER	3650		N	N	Y	N	N	
10	TLPRRGPRV	3651	12 LV10	N	Y	N	N	N	
9	LPXSF SIF	3652		N	N	N	N	Y	1
9	LPVCSF SIF	3653		N	N	N	N	Y	
9	LPXCSF SIF	3654		N	N	N	N	Y	
9	LPXCMF SIF	3655		N	N	N	N	Y	
9	LPXCSF SIF	3656		N	N	N	N	Y	
9	LPXCSF SIF	3657		N	N	N	N	Y	
9	LPXCSF SIF	3658		N	N	N	N	Y	
9	PPVWHGCP	3659		N	N	N	N	Y	
10	KPLTHGP TH	3660		N	N	N	N	Y	
10	APTLWARMI	3661		N	N	N	N	Y	
9	SPRASHPSI	3662		N	N	N	N	Y	No
10	LPKRGPRIG	3663		N	N	N	N	Y	
9	SPXQVEFI	3664		N	N	N	N	Y	
9	LPXCSF SIF	3665		N	N	N	N	Y	
9	DPFRSRRI	3666		N	N	N	N	Y	
10	SPGALVWGV	3667		N	N	N	N	Y	
10	TPLLYRLGAI	3668		N	N	N	N	Y	
9	TISGLWGV	3669		N	Y	N	N	N	
9	SISGLWGV	3670		N	Y	N	N	N	
9	SI MAFTASV	3671		N	Y	N	N	N	
9	GLPDCMLV	3672		N	Y	N	N	N	No
10	KI VALGVNAV	3673		N	Y	N	N	N	
10	HLPSRGPKL	3674		N	Y	N	N	N	
10	KISGLNAV	3675		N	Y	N	N	N	
10	VLPFRGPR	3676	LV2 110	N	Y	N	N	N	
10	VFRILGGW	3677		N	Y	N	N	N	
10	KVSLGVNAV	3678		N	Y	N	N	N	
9	CINGCWTIA	3679	12 VA9	N	Y	N	N	N	
9	CANFVCWTV	3680	1A2 V9	N	Y	N	N	N	

HCV ANALOGS

AA	Sequence	SeqID Num	Fixed Nomen	A1 Motif	A2 Super Motif	A3 Super Motif	A24 Motif	B7 Super Motif	1 Anchor Fixer
9	CVNGVCWAV	3681		N	Y	N	N	N	

Table XXIV. Human and murine MHC-peptide binding assays established using purified MHC molecules and gel filtration chromatography

Species		Antigen	Allele	Cell line	Radiolabeled peptide			Notes
					Source	Seq ID	Sequence	
Human	A1	A*0101	Steinlin	Hu J chain 102-110		3277	YIAVVTLY	no NEN in PI cocktail
	A2	A*0201	JY	HBBc 18-27 F6->Y		3278	FLPSDYTPSV	"
	A2	A*0202	P815 (transfected)	HBBc 18-27 F6->Y		3279	FLPSDYTPSV	"
	A2	A*0203	FUN	HBBc 18-27 F6->Y		3280	FLPSDYTPSV	"
	A2	A*0206	CLA	HBBc 18-27 F6->Y		3281	FLPSDYTPSV	"
	A2	A*0207	721.221 (transfected)	HBBc 18-27 F6->Y		3282	FLPSDYTPSV	"
	A3		GM3107	non-natural (A3CON1)		3283	KVEPYALINK	"
	A11		BVR	non-natural (A3CON1)		3284	KVEPYALINK	"
	A24	A*2402	KAS116	non-natural (A24CON1)		3285	AYIDNYNKF	"
	A31	A*3101	SPACH	non-natural (A3CON1)		3286	KVEPYALINK	"
	A33	A*3301	LWAGS	non-natural (A3CON1)		3287	KVEPYALINK	"
	A28/68	A*6801	C1R	HBBc 141-151 T7->Y		3288	STLPETYVVR	"
	A28/68	A*6802	AMAI	HBBc pol 646-654 C4->A		3289	FTQAGYPAL	"
	B7	B*0702	GM3107	A2 signal seq. 5-13 (L7->Y)		3290	APRTIAYLL	"
	B8	B*0801	Steinlin	HVgp 586-593 Y1->F, Q5->S		3291	ELKDYQLL	"
	B27	B*2705	LC2	R 60s		3292	FRYNGLIHR	"
	B35	B*3501	C1R, BVR	non-natural (B35CON2)		3293	FPIKYAAAF	"
	B35	B*3502	TISI	non-natural (B35CON2)		3294	FPIKYAAAF	"
	B35	B*3503	EHM	non-natural (B35CON2)		3295	FPIKYAAAF	"
	B44	B*4403	PTOUT	EF-1 C6->Y		3296	AEMGKYSFY	"
	B51		KAS116	non-natural (B35CON2)		3297	FPIKYAAAF	"
	B53	B*5301	AMAI	non-natural (B35CON2)		3298	FPIKYAAAF	"
	B54	B*5401	KT3	non-natural (B35CON2)		3299	FPIKYAAAF	"
	Cw4	Cw*0401	C1R	non-natural (C4CON1)		3300	QYDIDAVYKI	"
	Cw6	Cw*0602	721.221 transfected	non-natural (C6CON1)		3301	YRHDGQNVL	"
	Cw7	Cw*0702	721.221 transfected	non-natural (C6CON1)		3302	YRHDGQNVL	"
Mouse	D ^b		EL4	Adenovirus E1A P7->Y		3303	SGPSNTYPEI	"
	K ^b		EL4	VSV NP 52-59		3304	RGYVFCGL	"
	D ^d		P815	HIV-IIIb ENV G4->Y		3305	RCPYRAFVTI	"
	K ^d		P815	non-natural (KdCON1)		3306	KFNPMKLYI	"
	I ^d		P815	HIVs 28-39		3307	IPQSLDSYWTSL	"

Table XXIV. Human and murine MHC-peptide binding assays established using purified MHC molecules and gel filtration chromatography

Species	Antigen	Allele	Cell line	Radiolabeled peptide		Notes
				Source	Sequence	
Human	DR1	DRB1*0101	IC2	HA Y307-319	YPRYVKQNILKLTAT	optimal assay pH is 4.5
	DR2	DRB1*1501	I466.1	MBP 88-102V	VVHFFKNIVTPRTIPPY	
	DR2	DRB1*1601	I242.5	non-natural (760.16)	YAAFAAAKATAAAFA	
	DR3	DRB1*0301	MAT	MIT 65kD Y3-13	YKTIADFEEARR	
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT	
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAA	
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT	
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT	
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKHFEGITE	
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKHFEGITE	
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKHFEGITE	
	DR9	DRB1*0901	IID	Tet. tox. 830-843	QYIKANSKHFEGITE	
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKHFEGITE	
	DR12	DRB1*1201	Herluf	unknown eluted peptide	EALIHQLKINPYVLS	
	DR13	DRB1*1302	I40301	Tet. tox. 830-843 S->A	QYIKANAKHFEGITE	
	DR51	DRB5*0101	GM3107 or I416.3	Tet. tox. 830-843	QYIKANAKHFEGITE	
	DR51	DRB5*0201	I255.1	HA 307-319	PKYVKQNTLKLAT	
	DR52	DRB3*0101	MAT	Tet. tox. 1272-1284	NGQICNDPNRDIL	
	DR53	DRB4*0101	I257.6	non-natural (717.01)	YARFQSQTTLKQKT	
Mouse	DQ3.1	DQA1*0301/DQB1*0301	PF	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	no NEM in PI mix
	IA ^b		DR27.4	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	optimal assay pH is 5.5
	IA ^d		A20	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	
	IA ^e		CII-12	HEL 46-61	YNIDGSDYGLQINSR	optimal assay pH is 5.0
	IA ^c		LS102.9	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	
	IA ^a		91.7	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	
	II ^d		A20	Lambda repressor 12-26	YLEDARRPKAIYEKKK	optimal assay pH is 5.0
	II ^e		CII-12	Lambda repressor 12-26	YLEDARRPKAIYEKKK	optimal assay pH is 5.0

Table XXVI: HCV-derived conserved high algorithm A*0201-binding peptides

Peptide	Molecule	1st Position	Seq ID	Sequence	Consv.	A2-supertype binding capacity (IC 50 nM)					
						A*0201	A*0202	A*0203	A*0206	A*6802	A2 XRN
1073.05	NS4	1812	3335	LEFNILGGWV	85	4.2	113	3.2	19	33	5
1090.18	NS1/E2	728	3336	FLLADARV	92	18	90	149	247	111	5
1013.02	NS4	1590	3337	YLVAYQATV	85	20	39	16	82	33	5
1090.22	NS5	2611	3338	RLIVFPDLGV	79	56	391	10	370	8000	4
1013.1002	CORE	132	3339	DLMGYPLV	79	80	4778	204	481	12	4
24.0073	NS4	1920	3340	WMNRLLAFA	100	122	130	3.3	1609	400	4
24.0075	NS4	1666	3341	VLVCGVLA A	85	185	331	32	308	3077	4
1174.08	NS4	1769	3342	HIMWNILSGI	92	15	10750	77	132	7547	3
1073.06	NS4	1851	3343	ILAGYGAGV	79	116	143	5.0	755	889	3
1073.07	CORE	35	3344	YLLPRRCIPRL	92	125	6143	455	416	10256	3
24.0071	NS1/E2	726	3345	LEFLLADA	100	217	287	455	3364	3077	3
1.0119	LORF	1131	3346	YLVTRIADV	85	455	2048	3.6	71	3077	3
24.0065	NS4	1891	3347	ILSPGALVV	92	238	10750	27	1028	3077	2
1013.12	NS1/E2	686	3348	ALSTGLIHL	85	313	7167	45	18500	10256	2
939.14	NS1/E2	696	3349	HLHQNVIVDV	85	500	3071	19	1370	10811	2
1090.21	NS5	2918	3350	RLHGLSAFSL	79	179	782	625	18500	12500	1

Table XXVII: HCV-derived conserved high algorithm A*03 and/or A*11 binding peptides

Peptide	Molecule	1st Position	Seq ID	Sequence	Consv.	A3-supertype binding capacity (IC ₅₀ nM)						
						A*03	A*11	A*3101	A*3301	A*6801	A*3	XRN
1.0952	CORE	51	3364	KTSESRQPR	92	69	94	67	1813	145		4
1073.11	CORE	43	3365	RLGVRATRK	79	12	207	429	-	-		3
1.0955	ENV1	290	3366	QLFTFSPRR	79	15	182	621	3766	3		3
1073.13	NS1/E2	632	3367	RMVYVGVEHIR	100	15	300	95	9667	1778		3
1.0123	NS3	1396	3368	HLFCHSKKK	100	20	32	2535	24167	333		3
1073.10	NS4	1863	3369	GVAGALVAFK	85	28	4	3273	26364	118		3
24.0090	NS4	1864	3370	VAGALVAFK	85	46	7	3750	11600	258		3
24.0086	NS3	1262	3371	LGFGAYMSK	85	136	21	2950	22308	222		3
1174.16	NS1/E2	557	3372	WMNSTGFTK	79	208	74	12857	690	1429		2
1073.14	NS3	1261	3373	TLCFGAYMSK	85	136	98	-	22308	8889		2
1090.23	CORE	1183	3374	AVCTRGVAK	79	423	240	16364	-	-		2
1090.24	NS5	2596	3375	EVFCVQPEK	85	13750	222	-	-	18		2
24.0103	NS1/E2	647	3376	AACNWTRGLER	85	36667	429	400	5273	4444		2
1073.16	NS3	1232	3377	HLIAPTCSGK	85	19	2500	-	-	2857		1
1073.12	NS3	1395	3378	HLIFCHSKKK	100	423	-	20000	-	-		1
1090.26	NS3	1395	3379	HLIFCHSKKK	100	440	10000	-	-	8000		1

* A dash indicates IC₅₀nM >30,000

Table XXVIII: HCV derived conserved B*0702 binding peptides

A. High conservancy 9- and 10-mer peptides.

Peptide	Molecule	1st Position	SEQ ID	Sequence	Consv.	B7-supertypе binding capacity (IC50 nM)						
						B*0702	B*3501	B*51	B*5301	B*5401	B7 XRN	
1145.12	Core	169	3380	LPGCSFSIF	92	28	90	100	114	6667	4	
15.0048	E2	681	3381	LPALSTGLI	85	157	-	2.8	1500	20000	2	
15.0234	NS3	1620	3382	KPTLHGPTPL	79	3.9	-	27500	-	-	1	
15.0247	NS5	2835	3383	APTLWARMIL	79	6.3	-	5500	-	-	1	
15.0042	CORE	99	3384	SPRGSRPSW	79	14	-	11000	-	-	1	
15.0039	Core	57	3385	QPRGRRQPI	92	24	-	-	-	-	1	
15.0218	Core	37	3386	LPRRGPRIGV	92	29	-	6111	-	4000	1	
15.0060	NS5	2615	3387	SPGQRVEFL	79	46	-	27500	-	-	1	
15.0043	Core	111	3388	DPRRSRNL	85	324	-	-	-	-	1	
15.0063	NS5	2835	3389	APTLWARMI	79	344	-	4583	-	-	1	
1292.17	NS5	2317	3390	PPVVHGCPL	79	393	-	-	-	-	1	
15.0239	NS4	1893	3391	SPGALVVGAV	79	423	-	3438	-	-	1	
15.0235	NS3	1621	3392	TPLLYRLGAV	92	458	-	6875	-	909	1	

Table XXVIII: HCV derived conserved B*0702 binding peptides

B. Additional HCV derived B7 supermotif peptides.

Peptide	Molecule	1st Position	SEQ ID	Sequence	Consv.	B7-supertype binding capacity (IC ₅₀ nM)					
						B*0702	B*3501	B*51	B*5301	B*5401	B7 XRN
29.0035	NS3	1378	3393	IPFYGKAI	92	458	-	46	-	50	3
29.0040	Core	37	3394	LPRRGPRIL	92	0.85	-	306	-	5000	2
29.0036	Core	137	3395	IPLVGAPL	79	13	2250	79	-	2857	2
16.0187	NS1/E2	680	3396	LPGCSFTLPA	64	423	24000	9167	-	15	2
29.0039	Core	169	3397	LPGCSFSI	92	500	200	932	620	6250	2
15.0219	Core	142	3398	APLGGAAARAL	71	9.5	-	-	-	12500	1
29.0031	NS5	2869	3399	APTLWARM	79	13	-	4583	-	4348	1
15.0231	NS3	1512	3400	RPSGMFDSSV	71	153	-	-	-	-	1
29.0085	NS5	2474	3401	LPINALSNL	57	220	18000	1170	-	11111	1
29.0037	NS5	2608	3402	KPARLIVF	85	367	-	3235	-	16667	1
15.0237	NS4	1789	3403	NPAIASLMAF	71	393	9000	5000	-	-	1
29.0118	NS5	2869	3404	APTLWARMILM	79	423	-	-	-	3030	1
29.0042	NS4	1720	3405	LPYIEQGM	85	423	-	1375	-	7692	1

C. Engineered analogs of B7 supermotif peptides.

Peptide	Molecule	1st Position	SEQ ID	Sequence	Consv.	B7-supertype binding capacity (IC ₅₀ nM)					
						B*0702	B*3501	B*51	B*5301	B*5401	B7 XRN
1145.12	Core	169	3406	LPGCSFSIF	92	28	90	100	114	6667	4
1292.24	Core	169	3407	LPGCSFSII		37	4364	5.3	262	1056	3
1145.13	Core	169	3408	FPGCSFSIF		19	1.6	132	3.2	6.7	5

* A dash indicates IC₅₀ nM >30,000.

Table XXIX: HCV-derived A1- and A24-motif containing peptides**A. A1-motif peptides**

Peptide	Molecule	Position	Seq ID	Sequence	Conserv.	HLA-A*0101 binding (IC50 nM)
13.0019	NS5	2922	3409	LSAFSLHSY	79	31
1.0509	NS5	2921	3410	GLSAFSLHSY	79	61
1069.62	NS3	1128	3411	CTCGSSDLY	79	68
24.0093	NS5	2129	3412	EVDGVR LHRY	100	167
13.0016	NS3	1241	3413	KSTKVPAA Y	85	1923
1.0125	NS3	1525	3414	CYDAGCAWY	79	4032
24.0008	E1	206	3415	DCSNSSIVY	85	16667
24.0094	NS5	2720	3416	TNSKGQNCGY	100	-
24.0096	NS3	1240	3417	GKSTKVPAA Y	85	-
24.0100	NS3	1292	3418	TGAPITYSTY	85	-
	NS3	1263	3419	VAA TLGFGAY	100	
	NS5	2639	3420	VMGSSYGFQY	79	
	NS5	2640	3421	MGSSYGFQY	79	

A dash indicates IC50 nM >25000

B. A24 -motif peptides

Peptide	Molecule	Position	Seq ID	Sequence	Conserv.	HLA-A*2402 binding (IC50 nM)
24.0092	NS4	1765	3422	FWAKHMWNF	85	1.7
13.0075	NS4	1778	3423	QYLAGLSTL	100	250
1073.18	NS1 E2	636	3424	MYVGGVEHRL	92	444
13.0074	NS3	1297	3425	TYSTYGKFL	85	522
13.0134	NS5	2647	3426	QYSPGQRVEF	79	667
24.0091	NS4	1772	3427	NFISGIQYL	100	706
13.0131	Core	135	3428	GYIPLVGAPL	79	2105
24.0108	Core	173	3429	SFSIFLLALL	100	2927
13.0132	NS3	1248	3430	AYAAQGYKVL	79	13333
13.0133	NS4	1859	3431	GYGAGVAGAL	85	-
1174.08	NS4	1769	3432	HMWNFISGI	93	
	E1	317	3433	RMAWDMMMNW	85	
	NS1 E2	635	3434	RMVVGVEHRL	93	
	NS3	1422	3435	YYRGLDVSVI	100	
	NS3	1468	3436	DFSLDPTFTI	100	
	NS3	1608	3437	SWDQMWKCL	79	
	NS3	1664	3438	TWVLVGGVL	85	
	NS4	1732	3439	QFKQKALGL	85	
	NS4	1732	3440	QFKQKALGLL	85	
	NS4	1765	3441	FWAKHMWNFI	85	
	NS4	1919	3442	QWMNRLIAF	100	
	NS5	2241	3443	LWRQEMGGNI	85	
	NS5	2669	3444	GFSYDTRCF	79	
	NS5	2875	3445	RMILMTHFF	85	

A dash indicates IC50 nM >25000

Table XXX: Immunogenicity of A2-supertype cross-reactive binders

Peptide		Immunogenicity									
		Human ^a					Transgenic mice ^b				
		Seq ID	Sequence	Protein	Position	Barnaba; Barnaba; patients contacts	Chisari	Pape	overall	Frequency	Response
1073.05	3446	LLFNILGGWV	NS4	1812	1/6	7/17	2/21	0/6	10/50	6/6	6.4 (1.7)
1090.18	3447	FLLLADARV	NS1/E2	728	2/6	7/17	1/21	0/6	10/50	5/6	9.5 (3.0)
1013.02	3448	YLVAYQATV	NS4	1590	1/6	4/17	1/21	0/6	6/50	5/6	8.5 (3.7)
1090.22	3449	RLIVFPDGV	NS5	2578	2/6	5/17	0/21	0/6	7/50	0/6	-
1013.1002	3450	DLMGVPLV	Core	132	2/6	7/17	1/21	1/6	11/50	5/6	8.8 (2.6)
24.0073	3451	WMNRLLAF	NS4	1920	1/6	3/17	2/21	1/6	7/50	0/6	-
24.0075	3452	VLVGGVLA	NS4	1666	1/6	6/17	3/21	1/6	11/50	0/6	-
1174.08	3453	HMWNFSGI	NS4	1769	3/6	3/17	2/21	0/6	8/50	6/6	6.4 (1.7)
1073.06	3454	ILAGYGAGV	NS4	1851	2/6	3/17	0/21	0/6	5/50	3/6	54.7 (3.3)
1073.07	3455	YLLPRRGPR	CORE	35	2/6	5/17	7/21	1/6	17/50	4/6	59.1 (7.2)
24.0071	3456	LLFLLADA	NS1/E2	726	2/6	9/17	0/21	0/6	11/50	0/6	-
10119	3457	YLVTRHADV	NS3	1131	6/6	10/17	0/21	1/6	17/50	0/6	-

a. Data shown represents the number of positive responses over the total number of patients or contacts examined.

b. Frequency represents the number of positive responses over the total number of mice examined. Response indicates the average magnitude (standard deviation) of the response in positive animals, measured in lytic units.

Table XXXI: Immunogenicity of A3-supertype cross-reactive binders

Peptide	SEQ ID	Sequence	Protein	Position	Immunogenicity				
					Human ^a		Transgenic mice ^b		
					Barnaba patients	Barnaba contacts	Chisari	Pape	overall
1.0952	3458	KTSEESQPR	CORE	51	2/16	1/4	3/12	0/6	6/38
1073.11	3459	RLGVRAIRK	CORE	43	4/16	1/4	7/12	1/6	13/38
1.0955	3460	QLFTSPRR	ENV	290	1/16	0/4	6/12	1/6	8/38
1073.13	3461	RMYYVGGVTHR	NS142	632	5/16	1/4	4/12	1/6	11/38
1.0123	3462	LHCTHSKKK	NS3	1396	6/16	1/4	4/12	2/6	13/38
1073.10	3463	GVAGALVAFK	NS4	1863	3/16	0/4	6/12	2/6	11/38
24.0090	3464	VAGALVAFK	NS4	1864	4/16	1/4	6/12	0/4	11/38
24.0086	3465	TLGFGAYMSK	NS3	1262	6/16		2/12	2/5	10/33

a. Data shown represents the number of positive responses over the total number of patients or contacts examined.

b. Frequency represents the number of positive responses over the total number of mice examined. Response indicates the average magnitude (standard deviation) of the response in positive animals, measured in lytic units.

Table XXXII. Candidate HCV-derived HTL epitopes

Selection criteria	Peptide	SEQ ID	Sequence	Source	Conservancy	
					Total	Core
A DR-supermotif conserved 15mers	1283.01	3641	GQIVGGVYLLPRRGPR	HCV Core 28	93	93
	1283.02	3466	VYLLPRRGPRILGVRA	HCV Core 34	93	93
	1283.03	3467	GWLLSPRGSRPSWGPT	HCV Core 95	79	79
	1283.04	3468	LGKVIDTLTCGFADL	HCV Core 119	79	86
	1283.05	3469	IDTLTCGFADLMGYI	HCV Core 123	86	86
	1283.06	3470	ADLMGYIPLVGAPLG	HCV Core 131	79	79
	1283.07	3471	GVRVIEDGVNYATGN	HCV Core 154	86	86
	1283.08	3472	GVNYATGNLPGCSFS	HCV Core 161	79	86
	1283.09	3473	GCSFSIFLLALISCL	HCV Core 171	86	100
	1283.10	3474	GHRMAWDMMMNWSPT	HCV E1 315	86	86
	1283.11	3475	CGPVYCFETSPVYVG	HCV NS1 E2 506	93	93
	1283.12	3476	VYCFETSPVYVGTTD	HCV NS1 E2 509	93	93
	1283.13	3477	GNWFGCTWMNSTIGET	HCV NS1 E2 550	79	86
	1283.14	3478	FTTLPALSTGLIHLH	HCV NS1 E2 684	79	86
	1283.17	3479	DLYLVRHADVIPVR	HCV NS3 1134	79	79
	1283.18	3480	RAAVCTRGVAKAVDF	HCV NS3 1186	79	79
	1283.20	3481	AQGYKVI VLNPSVAA	HCV NS3 1251	79	100
	1283.21	3482	GYKVLVLNPSVAATL	HCV NS3 1253	100	100
	1283.22	3483	VLVLNPSVAATLGFG	HCV NS3 1256	100	100
	1283.23	3484	GTVLDAQETAGARLV	HCV NS3 1335	86	86
	1283.24	3485	GARLVVLAATATPPGS	HCV NS3 1345	79	86
	1283.25	3486	GRHLIFCHSKKKCDE	HCV NS3 1393	100	100
	1283.27	3487	DSVIDCNTCVTQTVD	HCV NS3 1454	86	86
	1283.28	3488	TVDFSLDPTFTIETI	HCV NS3 1466	79	100
	1283.30	3489	FTGLTHIDAHFLSQT	HCV NS3 1567	93	93
	1283.31	3490	YLVAYQATVCARAQA	HCV NS3 1591	79	93
	1283.32	3491	KPTLHGPTPLLYRLG	HCV NS4 1620	79	79
	1283.33	3492	LEVVTSTWVLVGGVL	HCV NS4 1658	86	86
	1283.34	3493	TWVLVGGVLAALAAY	HCV NS4 1664	86	86
	1283.35	3494	AEQFEKQKALGLQTA	HCV NS4 1730	86	86
	1283.40	3495	PAILSPGALVVGVCVA	HCV NS4 1889	79	93
	1283.41	3496	GALVVGVCVAAILRR	HCV NS4 1895	79	79
	1283.42	3497	CAAILRRHVGPGEGA	HCV NS4 1903	79	79
	1283.43	3498	AVQWMNRLIAFASRG	HCV NS4 1917	100	100
	1283.44	3499	MNRLIAFASRGNIHS	HCV NS4 1921	86	100
	1283.48	3500	ANLLWRQEMGGNITR	HCV NS5 2238	86	86
	1283.49	3501	RQEMGGNITRVESIN	HCV NS5 2243	86	86
	1283.52	3502	ARLIVFDELGVRVCE	HCV NS5 2610	79	79
	1283.53	3503	FPDLGVRVCEKMALY	HCV NS5 2615	79	100
	1283.54	3504	GVRVCEKMALYDVVS	HCV NS5 2619	79	100
	1283.56	3505	QPFYDI ELITSCSSN	HCV NS5 2808	79	93
	1283.57	3506	LELITSCSSNVSAH	HCV NS5 2813	79	100
	1283.58	3507	PTLWARMH MTHFES	HCV NS5 2870	79	86
	1283.59	3508	LHGISAFSLHSYSPG	HCV NS5 2919	79	79
	1283.60	3509	AFSLHSYSPGEINRV	HCV NS5 2924	79	79

Table XXXII. Candidate HCV-derived HTL epitopes

Selection criteria	Peptide	SEQ ID	Sequence	Source	Conservancy	
					Total	Core
B. High algorithm conserved core	1283.15	3510	VVLLFLLADARVCS	HCV NS1 E2-724	29	100
	1283.16	3511	SKGWRLLAPITAYAQ	HCV NS3 1025	29	79
	1283.19	3512	PQTFQVAHLHAPTGS	HCV NS3 1225	43	85
	1283.26	3513	DVVVVATDALMTGYT	HCV NS3 1436	43	79
	1283.29	3514	WESVFTGLTHIDAHF	HCV NS3 1563	43	92
	1283.45	3515	LTSMILTDPSHITAET	HCV NS5 2176	57	100
	1283.46	3516	ASQLSAPSLKATCTI	HCV NS5 2208	56	79
	1283.47	3517	DADLIEANLIWRQEM	HCV NS5 2232	50	85
	1283.50	3518	SYTWTGALITPCAAE	HCV NS5 2456	64	79
	1283.51	3519	TTIMAKNEVLCVQPE	HCV NS5 2589	64	85
	1283.55	3519	GSSYGFQYSPGQRVE	HCV NS5 2641	71	79
	1283.61	3521	ASCLRKLGVPPPLRVW	HCV NS5 2939	50	85
C. Collaborator	F098.03	3522	AAYAAQGYKVLVLPNSVAAT	HCV NS3 1242-1261	71	100
	F098.04	3523	GYKVLVLPNSVAATLGFAY	HCV NS3 1248-1267	100	
	F098.05	3524	GYKVLVLPNSVAAT	HCV NS3 1248-1261	100	
	F134.01	3525	RRPQDVKFPGGGQIVGGVY	HCV Core 17-35	86	
	F134.02	3526	DVKEPGGGQIVGGVYLLPRR	HCV Core 21-40	86	
	F134.03	3527	GYKVLVLPNSVAATLGFAY	HCV NS3 1253-1272	100	
	F134.04	3528	TLHGPTPLLYRLGAVQNEIT	HCV NS4 1622-1641		79
	F134.05	3529	NFISGIQYLAGLSTLPGNPA	HCV NS4 1772-1791	100	
	F134.06	3530	LLFNILGGWVAAQLAAPGAA	HCV NS4 1812-1831		86
	F134.07	3531	GPGEQAVQWMNRLIAFASRG	HCV NS4 1912-1931	86	100
	F134.08	3532	GEGAVQWMNRLIAFASRGNHV	HCV NS4 1914-1934	100	
	Pape 21	3533	AIPLEVYKGGRHILFCHSKR	HCV NS3 1379-1398	21	100
	Pape 22	3534	GRHLIFCHSKRKCDELATKL	HCV NS3 1388-1407		100
D. DR3 motif	Pape 29	3535	SVIDCNTCVTQTVDFSLDPT	HCV NS3 1450-1469	86	
	35.0102	3536	GVRVLEDGVNYATGN	HCV 154	86	86
	35.0103	3537	SAMYVGDLCSVTLV	HCV 273	57	86
	35.0104	3538	GHRMAWDMMMNWSPT	HCV 315	86	86
	35.0105	3539	SDLYLVTRHADVIPV	HCV 1133	79	86
	35.0106	3540	VVVVATDALMTGYTG	HCV 1437	42	86
	35.0107	3541	TVDFSLDPTFTIETI	HCV 1466	79	100
	35.0108	3542	DSSVLCECYDAGCAW	HCV 1518	71	93
	35.0109	3543	GLPVCQDHLFEWESV	HCV 1552	42	86
	35.0110	3544	GMQLAEQFKQKALGL	HCV 1726	57	86
	35.0111	3545	PTHYVPESDAARVT	HCV 1936	86	86
	35.0112	3546	GSQLPCEPEPDVAVL	HCV 2162	64	86
	35.0113	3547	LTSMILTDPSHITAET	HCV 2176	57	100
	35.0114	3548	MPPLFEGEPDPLSD	HCV 2401	79	100
	35.0115	3549	QPEYDLELITSCSSN	HCV 2808	79	93
	1283.25	3550	GRHLIFCHSKRKCDEL	HCV NS3 1393-1407		

Table XXXIV. HLA-DR binding capacity of target derived peptides: DR-supermotif and algorithm positive peptides.

Peptide	SEQ ID	Sequence	Source	Binding capacity (IC50 nM)											DR alleles	
				DR1	DR2w2B1	DR2w2B2	DR4w4	DR4w15	DR5w11	DR6w19	DR7	DR8w2	DR9	IAb	bound	
	3551	AAVAAQGYKVI	VI NPSVAAII GFGAY	HCV NS3 1242-1267												
1283.21	3552	GYKVI	VI NPSVAAII	HCV NS3 1253	4.5	350	-	5.2	567	143	5.1	89	288	54	175	9
1283.20	3553	AGGYKVI	VI NPSVAA	HCV NS3 1251	6.0	650	-	7.9	224	74	5.9	833	175	375	298	9
198.03	3554	AAVAAQGYKVI	VI NPSVAAI	HCV NS3 1242	2.9	48	483	18	1234	103	11	96	60	240		9
198.05	3555	GYKVI	VI NPSVAAI	HCV NS3 1248-1261	1.4	39	3695	7.8	141	75	3.5	126	21	266		9
198.04	3556	GYKVI	VI NPSVAAII GFGAY	HCV NS3 1248-1267	3.5	42	8154	9.7	1500	240	4.1	23	80	20		8
	3557	GFGAVQWMNRI	IATASRGNIHS	HCV NS4 1914-1935												
1283.44	3558	MINRI	IATASRGNIHS	HCV NS4 1921	66	4.8	1538	6329	585	45	7.3	227	102	313	147	8
1134.08	3559	GFGAVQWMNRI	IATASRGNIHV	HCV NS4 1914	3.2		182	361		345		221	158	6818		6
1283.16	3560	SKGAWRI	LAPITAYAQ	HCV NS3 1025	0.36	125	23	24	152	4.8	-	962	54	1190	384	8
1283.55	3561	GSSYGTQYSPGQRVE		HCV NS5 2641	11	-	667	417	745	20000	19	156	-	68	571	7
1283.61	3562	ASGTRKLGVPPI	RVW	HCV NS5 2939	5.0	16	217	6250	78	645	2500	862	671	8621	-	7
1134.05	3563	NIISGIGYI	AGLSII PGNPA	HCV NS4 1772	10		606	84		29		-	70	441		6

Shading indicates IC₅₀ < 1 μM

A dash (-) indicates IC₅₀ > 20 μM

Table XXXV. HLA-DR binding capacity of 3 DR3 motif-containing peptides

Peptide	Seq #	Sequence	Source	DR3 binding* (IC ₅₀ nM)
35.0106	3564	VVVVATDAlMTGYTG	HCV 1437	427
35.0107	3565	TVDFSLDPTFTIETT	HCV 1466	235
1283.25	3566	GRIILIFCTISKKKCDE	HCV NS3 1393	ND

Table XXXVIa: HCV-derived CTL epitope candidates

Peptide	Molecule	1st Position	Seq ID	Sequence	Consv.	Selection criteria
1073.05	NS4	1812	3567	LLFNILGGWV	85	A2-supertype
1090.18	NS1/E2	728	3568	FLLADARV	92	A2-supertype
1013.02	NS4	1590	3569	YLVAYQATV	85	A2-supertype
1090.22	NS5	2611	3570	RLIVFDLGV	79	A2-supertype
1013.1002	CORE	132	3571	DLMGYPLV	79	A2-supertype
24.0073	NS4	1920	3572	WMNRLIAFA	100	A2-supertype
24.0075	NS4	1666	3573	VLVGGVLA	85	A2-supertype
1174.08	NS4	1769	3574	IIMWNFSCI	92	A2-supertype
1073.06	NS4	1851	3575	ILAGYGAGV	79	A2-supertype
1073.07	CORE	35	3576	YLLPRRGPR	92	A2-supertype
24.0071	NS1/E2	726	3577	LLFLLADA	100	A2-supertype
1.0119	LORF	1131	3578	YLVTRHADV	85	A2-supertype
1.0952	CORE	51	3579	KTSESRQPR	92	A3-supertype
1073.11	CORE	43	3580	RLGVRATRK	79	A3-supertype
1.0955	ENV1	290	3581	QLFTESPRR	79	A3-supertype
1073.13	NS1/E2	632	3582	RMVVGVEHR	100	A3-supertype
1.0123	NS3	1396	3583	LIFCHSKKK	100	A3-supertype
1073.10	NS4	1863	3584	GVAGALVAFK	85	A3-supertype
24.0090	NS4	1864	3585	VAGALVAFK	85	A3-supertype
24.0086	NS3	1262	3586	TLGFGAYMSK	85	A3-supertype
F104.01	NS5	3003	3587	VGIVLLPNR	79	A31
1145.12	Core	169	3588	LPGCSFSIF	92	B7-supertype
29.0035	NS3	1378	3589	IPFYGKAI	92	B7-supertype
13.0019	NS5	2922	3590	LSAFSLHSY	79	A1
1069.62	NS3	1128	3591	CTCGSSDIY	79	A1
24.0092	NS4	1765	3592	FWAKIMWNF	85	A24

Table XXXVIIb. HCV-derived HTL epitope candidates

Region	Peptide	Motif ¹	Seq ID	Sequence
HCV NS3 1025-1039	1283.16	DR	3593	SKGWRLLAPITAYAQ
HCV NS3 1242-1267	F98.03	DR	3594	AAVAAQGYKVLVLNPSVAAT
HCV NS3 1393-1407	1283.25	DR3	3595	GRHLIRCHSKKKCDE
HCV NS3 1437-1451	35.0106	DR3	3596	VVVVATDALMTGYTG
HCV NS3 1466-1480	35.0107	DR3	3597	TVDFSLDPTFTIETT
HCV NS4 1772-1790	F134.05	DR	3598	NFISCIQYLAGLSTLPCNPA
HCV NS4 1914-1935	F134.08	DR	3599	GEGAVQWMNRUIAFASRGNIIV
HCV NS5 2641-2655	1283.55	DR	3600	GSSYGFQYSPGQRVE
HCV NS5 2939-2953	1283.61	DR	3601	ASCLRKLGVPPLRVW

1. Peptides identified on the basis of either the DR P1-P6 supermotif or by use of the DR1-4-7 algorithms are indicated by 'DR'. Peptides identified using the DR3 motif are indicated by 'DR3'.

Table XXXVII. Estimated population coverage by a panel of HCV derived HTL epitopes

Antigen	Alleles	Representative assay	No. of epitopes ²	Population coverage (phenotypic frequency)					
				Cauc.	Blk.	Jpn.	Chn.	Hisp.	Avg.
DR1	DRB1*0101-03	DR1	6	18.5	8.4	10.7	4.5	10.1	10.4
DR2	DRB1*1501-03	DR2w2 B1	3	19.9	14.8	30.9	22.0	15.0	20.5
DR2	DRB5*0101	DR2w2 B2	6	-	-	-	-	-	-
DR3	DRB1*0301-2	DR3	2	17.7	19.5	0.40	7.3	14.4	11.9
DR4	DRB1*0401-12	DR4w4	5	23.6	6.1	40.4	21.9	29.8	24.4
DR4	DRB1*0401-12	DR4w15	3	-	-	-	-	-	-
DR7	DRB1*0701-02	DR7	5	26.2	11.1	1.0	15.0	16.6	14.0
DR8	DRB1*0801-5	DR8w2	5	5.5	10.9	25.0	10.7	23.3	15.1
DR9	DRB1*09011,09012	DR9	3	3.6	4.7	24.5	19.9	6.7	11.9
DR11	DRB1*1101-05	DR5w11	5	17.0	18.0	4.9	19.4	18.1	15.5
DR13	DRB1*1301-06	DR6w19	2	21.7	16.5	14.6	12.2	10.5	15.1
Total				98.5	95.1	97.1	91.3	94.3	95.1

1. Total population coverage has been adjusted to account for the presence of DRX in many ethnic populations. It has been assumed that the range of specificities represented by DRX alleles will mirror those of previously characterized HLA-DR alleles. The proportion of DRX incorporated under each motif is representative of the frequency of the motif in the remainder of the population. Total coverage has not been adjusted to account for unknown gene types.

2. Number of epitopes represents a minimal estimate, considering only the epitopes shown in Table 6. Additional alleles possibly bound by nested epitopes have not been accounted.